Please amend the application as follows.

IN THE SPECIFICATION:

Please amend the specification in accordance with § 1.52(e)(5) and § 1.77(b)(4) at page 1, line 35 following the Statement Regarding Federally Sponsored Research or Development to include the following paragraph:

--The Sequence Listing written in file 141ultra.txt, 2,439,302 bytes, created on November 15, 2000 on two identical copies of compact discs for Application No: 09/412,863, Sette *et al.*, Inducing Cellular Immune Responses To Human Immunodeficiency Virus-1 Using Peptide And Nucleic Acid Compositions, is hereby incorporated by reference.--

Please delete each page of Tables IV, V, IX, XX, XXIII, XXIV, XXVII-XXXIII, and XXXV-XXXIX and insert therefor each page of the replacement Tables IV, V, IX, XX, XXIII, XXIV, XXVII-XXXIII, and XXXV-XXXIX submitted herewith.

On page 52, line 3, after 'QYIKANSKFIGITE', please insert --; SEQ ID NO:14488--.

On page 52 line 4, after 'DIEKKIAKMEKASSVFNVVNS', please insert --; SEQ ID NO:14489--.

On page 52 line 5, after 'GAVDSILGGVATYGAA', please insert --; SEQ ID NO:14490--.

On page 52, line 12, after 'aKXVWANTLKAAa', please insert --(SEQ ID NO: 14491)--.

The amendment to the specification adds no new matter. The amendment sets out the SEQ ID NOs. for sequences present in the application as filed.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

Jean M. Lockyer
Reg. No. 44,879

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JML/mcd
SF 1160805 v1

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQ ID	SEQUENCE	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	14492	YLEPAIAKY	25
A*0201	941.01	14493	FLPSDYFPSV	5.0
A*0202	941.01	14494	FLPSDYFPSV	4.3
A*0203	941.01	14495	FLPSDYFPSV	10
A*0205	941.01	14496	FLPSDYFPSV	4.3
A*0206	941.01	14497	FLPSDYFPSV	3.7
A*0207	941.01	14498	FLPSDYFPSV	23
A*6802	1141.02	14499	FTQAGYPAL	40
A*0301	941.12	14500	KVFPYALINK	11
A*1101	940.06	14501	AVDLYHFLK	6.0
A*3101	941.12	14502	KVFPYALINK	18
A*3301	1083.02	14503	STLPETYVVRR	29
A*6801	941.12	14504	KVFPYALINK	8.0
A*2402	979.02	14505	AYIDNYNKF	12
B*0702	1075.23	14506	APRTLVYLL	5.5
B*3501	1021.05	14507	FPFKYAAAF	7.2
B51	1021.05	14508	FPFKYAAAF	5.5
B*5301	1021.05	14509	FPFKYAAAF	9.3
B*5401	1021.05	14510	FPFKYAAAF	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	SEQ ID	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	14511	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	14512	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	14513	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	14514	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	14515	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	14516	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	14517	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	14518	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	14519	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	14520	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	14521	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	14522	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2β1	507.02	14523	GRTQDENPVVHFFK NIVTPRTPPP	9.1
DRB3*0101	DR52a	511	14524	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	14525	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2β2	553.01	14526	QYIKANSKFIGITE	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table XIXa

HIV DR Super Motif Peptides

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	VSTQLLLNG	13520	61	95	KPVVSTQLLLNGSLA	12864	299	29	45
ENV	VVSTQLLLN	13521	60	94	IKPVVSTQLLLNGSL	12865	298	29	45
ENV	LTVWGIKQL	13522	59	92	LLQLTVWGIKQLQAR	12866	651	26	41
ENV	LLSGIVQQQ	13523	58	91	ARQLLSGIVQQQSNL	12867	627	22	34
ENV	WATHACVPT	13524	56	88	HNVWATHACVPTDPN	12868	79	44	69
ENV	LGAAGSTMG	13525	55	86	LGFLGAAGSTMGAAS	12869	605	36	56
ENV	VRQGYSPLS	13526	55	86	VNRVRQGYSPLSFQT	12870	800	36	57
ENV	LLLNGSLAE	13527	54	84	STQLLLNGSLAEEEV	12871	303	16	25
ENV	VKLTPLCVT	13528	53	83	KPCVKLTPLCVTLNC	12872	130	29	45
ENV	LRAIEAQQH	13529	51	80	NNLLRAIEAQQHLLQ	12873	639	18	28
ENV	VSTVQCTHG	13530	51	80	CKNVSTVQCTHGIKP	12874	285	14	22
ENV	LGIWGCSGK	13531	50	78	QQLLGIWGCSGKLIC	12875	676	46	72
ENV	LWDQSLKPC	13532	50	78	IISLWDQSLKPCVKL	12876	121	35	55
ENV	LGFLGAAGS	13533	49	77	AVFLGFLGAAGSTMG	12877	602	19	30
ENV	VWATHACVP	13534	49	77	VHNVWATHACVPTDP	12878	78	34	53
ENV	WGIKQLQAR	13535	49	77	LTVWGIKQLQARVLA	12879	654	39	61
ENV	LWYIKIFIM	13536	43	67	TNWLWYIKIFIMIVG	12880	771	11	17
ENV	FCASDAKAY	13537	42	66	TTLFCASDAKAYDTE	12881	61	18	28
ENV	IVGGLIGLR	13538	42	66	FIMIVGGLIGLRIVF	12882	780	22	34
ENV	IFIMIVGGL	13539	41	64	YIKIFIMIVGGLIGL	12883	776	30	47
ENV	VYYGVPVWK	13540	41	64	WVTVYYGVPVWKEAT	12884	46	22	34
ENV	IKQLQARVL	13541	40	63	VWGIKQLQARVLAVE	12885	656	31	49
ENV	IKIFIMIVG	13542	39	61	LWYIKIFIMIVGGLI	12886	774	31	48
ENV	MGAASITLT	13543	39	61	GSTMGAASITLTVQA	12887	613	28	44
ENV	YIKIFIMIV	13544	39	61	WLWYIKIFIMIVGGL	12888	773	38	59
ENV	ITGLLLTRD	13545	37	58	SSNITGLLLTRDGGK	12889	516	06	9
ENV	IPIHYCAPA	13546	36	56	FEPIPIHYCAPAGFA	12890	255	21	33
ENV	MIVGGLIGL	13547	36	56	IFIMIVGGLIGLRIV	12891	779	22	34
ENV	VQARQLLSG	13548	36	56	TLTVQARQLLSGIVQ	12892	622	35	55
ENV	FEPIPIHYC	13549	35	55	KVSFEPIPIHYCAPA	12893	252	17	27
ENV	LRSLCLFSY	13550	35	55	WDDLRSLCLFSYHRL	12894	854	28	44
ENV	MWKNNMVEQ	13551	35	55	NFNMWKNNMVEQMHE	12895	105	11	17
ENV	VHNVWATHA	13552	35	55	DTEVHNVWATHACVP	12896	75	17	27
ENV	WKNNMVEQM	13553	35	55	FNMWKNNMVEQMHED	12897	106	20	31
ENV	YYGVPVWKE	13554	35	55	VTVYYGVPVWKEATT	12898	47	22	34
ENV	LLQLTVWGI	13555	34	53	QQHLLQLTVWGIKQL	12899	648	34	53
ENV	IEPLGVAPT	13556	33	52	VVKIEPLGVAPTKAK	12900	566	12	19
ENV	IKPVVSTQL	13557	33	52	THGIKPVVSTQLLLN	12901	295	32	50
ENV	LQARVLAVE	13558	33	52	IKQLQARVLAVERYL	12902	659	32	50
ENV	WDDLRSLCL	13559	33	52	ALAWDDLRSLCLFSY	12903	851	18	28
ENV	IINIHTPHR	13560	01	50	SRPIINIHTPHREKR	12904	581	01	2
ENV	INIHTPHRE	13561	01	50	RPIINIHTPHREKRA	12905	582	01	2
ENV	ITQACPKVS	13562	32	50	TSVITQACPKVSFEP	12906	242	08	13
ENV	IVQQQSNLL	13563	32	50	LSGIVQQQSNLLRAI	12907	631	26	41
ENV	LGNNSTNST	13564	01	50	NKTLGNNSTNSTLGN	12908	151	01	2
ENV	VISTRTHRE	13565	01	50	ARPVISTRTHREKRA	12909	580	01	2
ENV	WRWGTLFLG	13566	01	50	QNLWRWGTLFLGMLM	12910	12	01	2
ENV	WRWGTMLLG	13567	01	50	QHLWRWGTMLLGMLM	12911	12	03	5
ENV	FAVLSIVNR	13568	31	48	RIVFAVLSIVNRVRQ	12912	791	14	22
ENV	LLNGSLAEE	13569	31	48	TQLLLNGSLAEEEVV	12913	304	14	22

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	LTPLCVTLN	13570	29	45	CVKLTPLCVTLNCTD	12914	132	11	17
ENV	LYKYKVVKI	13571	29	45	RSELYKYKVVKIEPL	12915	558	23	36
ENV	VPWNSSWSN	13572	29	45	TTNVPWNSSWSNKSL	12916	691	03	5
ENV	YRLINCNTS	13573	28	44	YKEYRLINCNTSAIT	12917	232	01	8
ENV	IHYCAPAGF	13574	27	42	PIPIHYCAPAGFAIL	12918	258	26	41
ENV	LKDQQLLGI	13575	27	42	ERYLKDQQLLGIWGC	12919	670	25	39
ENV	YKYKVVKIE	13576	27	42	SELYKYKVVKIEPLG	12920	559	24	38
ENV	IRPVVSTQL	13577	26	41	THGIRPVVSTQLLLN	12921	295	26	41
ENV	LDKWASLWN	13578	26	41	LLALDKWASLWNWFD	12922	755	08	13
ENV	LRIVFAVLS	13579	26	41	LIGLRIVFAVLSIVN	12923	787	10	16
ENV	LNGSLAEEE	13580	25	39	QLLLNGSLAEEEVVI	12924	305	13	20
ENV	YKVVKIEPL	13581	25	39	LYKYKVVKIEPLGVA	12925	561	23	36
ENV	LKGLRLGWE	13582	11	37	RSSLKGLRLGWEGLK	12926	885	04	7
ENV	FSYHRLRDL	13583	23	36	LCLFSYHRLRDLLLI	12927	860	08	13
ENV	INCTRPNNN	13584	23	36	SVEINCTRPNNNTRK	12928	340	05	8
ENV	VVKIEPLGV	13585	23	36	KYKVVKIEPLGVAPT	12929	563	23	36
ENV	WKEATTTLF	13586	23	36	VPVWKEATTTLFCAS	12930	53	22	34
ENV	IGLRIVFAV	13587	22	34	GGLIGLRIVFAVLSI	12931	785	12	19
ENV	FFYCNTSGL	13588	21	33	GGEFFYCNTSGLFNS	12932	441	07	11
ENV	FGLGALFLG	13589	01	33	RAAFGLGALFLGFLG	12933	594	01	2
ENV	FYCNTSGLF	13590	21	33	GEFFYCNTSGLFNST	12934	442	07	11
ENV	LIGLRIVFA	13591	21	33	VGGLIGLRIVFAVLS	12935	784	17	27
ENV	VGLGAVFLG	13592	01	33	KRAVGLGAVFLGFLG	12936	593	06	9
ENV	VGLGMLFLG	13593	01	33	KRAVGLGMLFLGVLS	12937	594	01	2
ENV	ICTTAVPWN	13594	20	31	GKLICTTAVPWNSSW	12938	686	09	14
ENV	ICTTNVPWN	13595	20	31	GKLICTTNVPWNSSW	12939	686	08	13
ENV	LGVAPTKAK	13596	19	30	IEPLGVAPTKAKRRV	12940	569	15	23
ENV	LICTTAVPW	13597	19	30	SGKLICTTAVPWNSS	12941	685	09	14
ENV	LRDQQLLGI	13598	19	30	ERYLRDQQLLGIWGC	12942	670	17	27
ENV	VFLGFLGAA	13599	19	30	LGAVFLGFLGAAGST	12943	600	09	14
ENV	FSYHRLRDF	13600	18	28	LCLFSYHRLRDFILI	12944	860	08	13
ENV	IPIHYCTPA	13601	18	28	FEPIPIHYCTPAGFA	12945	255	10	16
ENV	IVFAVLSIV	13602	18	28	GLRIVFAVLSIVNRV	12946	789	16	25
ENV	VFAVLSIVN	13603	18	28	LRIVFAVLSIVNRVR	12947	790	16	25
ENV	VPWNASWSN	13604	18	28	TTAVPWNASWSNKSL	12948	691	06	9
ENV	IGLRIIFAV	13605	17	27	GGLIGLRIIFAVLSI	12949	785	11	17
ENV	IRQAHCNIS	13606	17	27	IGDIRQAHCNISRAK	12950	378	02	3
ENV	VAPTKAKRR	13607	17	27	PLGVAPTKAKRRVVQ	12951	571	10	16
ENV	FNGTGPCKN	13608	16	25	DKKFNGTGPCKNVST	12952	276	05	8
ENV	IGPGQTFYA	13609	01	25	SVRIGPGQTFYATGD	12953	355	03	5
ENV	IGSGQAFYV	13610	01	25	RYSIGSGQAFYVTGK	12954	358	01	2
ENV	IRYLNLVNQ	13611	01	25	QTAIRYLNLVNQTEN	12955	400	01	2
ENV	LIGLRIIFA	13612	16	25	VGGLIGLRIIFAVLS	12956	784	12	19
ENV	LLQYWSQEL	13613	16	25	WWNLLQYWSQELKNS	12957	903	09	14
ENV	LRNLCLFSY	13614	16	25	WDDLRNLCLFSYHRL	12958	854	11	17
ENV	LVSGFLALA	13615	16	25	SIRLVSGFLALAWDD	12959	842	09	14
ENV	VSGFLALAW	13616	16	25	IRLVSGFLALAWDDL	12960	843	09	14
ENV	FDPIPIHYC	13617	15	23	KVTFDPIPIHYCTPA	12961	252	03	5
ENV	IIFAVLSIV	13618	15	23	GLRIIFAVLSIVNRV	12962	789	13	20
ENV	LINCNTSAI	13619	15	23	EYRLINCNTSAITQA	12963	234	04	9

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	LLNATAIAV	13620	15	23	AVSLLNATAIAVAEG	12964	918	10	16
ENV	LRIIFAVLS	13621	15	23	LIGLRIIFAVLSIVN	12965	787	11	17
ENV	VITQACPKV	13622	15	23	NTSVITQACPKVSFE	12966	241	08	13
ENV	YWWNLLQYW	13623	15	23	VLKYWWNLLQYWSQE	12967	899	07	11
ENV	FAILKCNDK	13624	14	22	PAGFAILKCNDKKFN	12968	266	09	14
ENV	IFAVLSIVN	13625	14	22	LRIIFAVLSIVNRVR	12969	790	13	20
ENV	INCNTSAIT	13626	14	22	YRLINCNTSAITQAC	12970	235	14	22
ENV	LNATAIAVA	13627	14	22	VSLLNATAIAVAEGT	12971	919	10	16
ENV	WNSSWSNKS	13628	14	22	NVPWNSSWSNKSLDE	12972	693	03	5
ENV	WNASWSNKS	13629	13	21	NVPWNASWSNKSYED	12973	693	02	3
ENV	ICTTTVPWN	13630	13	20	GKLICTTTVPWNASW	12974	686	06	9
ENV	LLKLTVWGI	13631	13	20	QQHLLKLTVWGIKQL	12975	648	13	20
ENV	LYKYKVVEI	13632	13	20	RSELYKYKVVEIKPL	12976	558	05	8
ENV	MFLGFLGAA	13633	13	20	LGAMFLGFLGAAGST	12977	600	07	11
ENV	MHSFNCGGE	13634	13	20	EIVMHSFNCGGEFFY	12978	430	13	20
ENV	YWSQELKNS	13635	13	20	LLQYWSQELKNSAVS	12979	906	10	16
ENV	IGAVFLGFL	13636	12	19	AVGIGAVFLGFLGAA	12980	595	09	14
ENV	LIAARTVEL	13637	12	19	DFILIAARTVELLGH	12981	870	04	6
ENV	LICTTTVPW	13638	12	19	SGKLICTTTVPWNAS	12982	685	06	9
ENV	LLNGSLAEG	13639	12	19	TQLLLNGSLAEGEII	12983	304	03	5
ENV	YWGQELKNS	13640	12	19	LVWYWGQELKNSAIS	12984	906	02	3
ENV	IAARTVELL	13641	11	17	FILIAARTVELLGHS	12985	871	03	5
ENV	LFLGFLGAA	13642	11	17	IGALFLGFLGAAGST	12986	600	06	9
ENV	LKNSAVSLL	13643	11	17	SQELKNSAVSLLNAT	12987	911	08	13
ENV	VGIGAVFLG	13644	11	17	KRAVGIGAVFLGFLG	12988	593	11	17
ENV	VSLLNATAI	13645	11	17	NSAVSLLNATAIAVA	12989	916	09	14
ENV	YATGDIIGD	13646	11	17	QTFYATGDIIGDIRQ	12990	365	04	6
ENV	IAIAVAEGT	13647	10	16	LDIIAIAVAEGTDRI	12991	922	02	3
ENV	IHYCTPAGF	13648	10	16	PIPIHYCTPAGFAIL	12992	258	08	13
ENV	ILGLVIICS	13649	10	16	GTLILGLVIICSASN	12993	19	03	5
ENV	IWNNMTWME	13650	10	16	VDEIWNNMTWMEWER	12994	714	01	2
ENV	LGLVIICSA	13651	10	16	TLILGLVIICSASNN	12995	20	04	6
ENV	LRDFILIAA	13652	10	16	YHRLRDFILIAARTV	12996	865	06	9
ENV	LTPLCVTLD	13653	10	16	CVKLTPLCVTLDCHN	12997	132	03	5
ENV	MLQLTVWGI	13654	10	16	QQHMLQLTVWGIKQL	12998	648	08	13
ENV	VEINCTRPN	13655	10	16	NESVEINCTRPNNNT	12999	338	02	3
ENV	VRQLLSGIV	13656	10	16	TVQVRQLLSGIVQQQ	13000	624	08	13
ENV	LILGLVIIC	13657	09	15	WGTLILGLVIICSAS	13001	18	07	11
GAG	VGGHQAAMQ	13658	60	94	LNTVGGHQAAMQMLK	13002	209	47	73
GAG	LLVQNANPD	13659	59	92	TETLLVQNANPDCKT	13003	342	26	41
GAG	VQNANPDCK	13660	59	92	TLLVQNANPDCKTIL	13004	344	44	69
GAG	LGLNKIVRM	13661	58	91	WIILGLNKIVRMYSP	13005	289	55	86
GAG	LSEGATPQD	13662	58	91	FSALSEGATPQDLNT	13006	193	29	45
GAG	WIILGLNKI	13663	57	89	YKRWIILGLNKIVRM	13007	286	54	84
GAG	LEEMMTACQ	13664	56	88	GATLEEMMTACQGVG	13008	364	27	42
GAG	YKRWIILGL	13665	55	86	GEIYKRWIILGLNKI	13009	283	37	58
GAG	IYKRWIILG	13666	54	84	VGEIYKRWIILGLNK	13010	282	37	58
GAG	VSQNYPIVQ	13667	48	83	SSQVSQNYPIVQNLQ	13011	145	09	19
GAG	WEKIRLRPG	13668	50	78	LDKWEKIRLRPGGKK	13012	13	16	25
GAG	IAGTTSTLQ	13669	46	72	GSDIAGTTSTLQEQI	13013	254	45	70

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
GAG	WASRELERF	13670	46	72	HLVWASRELERFALN	13014	34	17	27
GAG	IPMFSALSE	13671	45	70	PEVIPMFSALSEGAT	13015	187	44	69
GAG	MFSALSEGA	13672	45	70	VIPMFSALSEGATPQ	13016	189	43	67
GAG	VIPMFSALS	13673	45	70	SPEVIPMFSALSEGA	13017	186	40	63
GAG	MYSPVSILD	13674	41	64	IVRMYSPVSILDIRQ	13018	297	23	36
GAG	IVRMYSPVS	13675	40	63	LNKIVRMYSPVSILD	13019	294	39	61
GAG	VRMYSPVSI	13676	40	63	NKIVRMYSPVSILDI	13020	295	38	59
GAG	YSPVSILDI	13677	40	63	VRMYSPVSILDIRQG	13021	298	23	36
GAG	MTETLLVQN	13678	38	59	KNWMTETLLVQNANP	13022	338	34	53
GAG	WMTETLLVQ	13679	37	58	VKNWMTETLLVQNAN	13023	337	34	53
GAG	ISPRTLNAW	13680	36	56	HQAISPRTLNAWVKV	13024	165	27	42
GAG	VKNWMTETL	13681	36	56	TQEVKNWMTETLLVQ	13025	334	14	22
GAG	IKCFNCGKE	13682	34	53	QKRIKCFNCGKEGHL	13026	418	05	8
GAG	IPVGEIYKR	13683	34	53	NPPIPVGEIYKRWII	13027	277	32	51
GAG	YTAVFMQRG	13684	02	50	KGGYTAVFMQRGQNP	13028	399	02	3
GAG	VATLYCVHQ	13685	30	47	YNTVATLYCVHQRIE	13029	81	07	11
GAG	WDRLHPVHA	13686	29	45	AAEWDRLHPVHAGPI	13030	230	22	34
GAG	FLQSRPEPT	13687	28	44	PGNFLQSRPEPTAPP	13031	483	27	43
GAG	FKTLRAEQA	13688	27	42	DRFFKTLRAEQATQE	13032	322	16	25
GAG	MVIIQAISPR	13689	27	42	QGQMVHQAISPRTLN	13033	160	26	41
GAG	VHQAISPRT	13690	27	42	GQMVHQAISPRTLNA	13034	161	27	42
GAG	YKTLRAEQA	13691	27	42	DRFYKTLRAEQASQE	13035	322	12	19
GAG	VSILDIRQG	13692	25	39	YSPVSILDIRQGPKE	13036	301	24	38
GAG	LAEAMSQVT	13693	23	37	ARVLAEAMSQVTNSA	13037	384	08	13
GAG	LGKIWPSHK	13694	23	36	ANFLGKIWPSHKGRP	13038	467	22	34
GAG	VKCFNCGKE	13695	23	36	RKTVKCFNCGKEGHI	13039	420	07	11
GAG	YNTVATLYC	13696	23	36	RSLYNTVATLYCVHQ	13040	78	11	17
GAG	LHPVHAGPI	13697	22	34	WDRLHPVHAGPIAPG	13041	233	15	23
GAG	LYNTVATLY	13698	22	34	LRSLYNTVATLYCVH	13042	77	13	20
GAG	MTDTLLVQN	13699	22	34	KNWMTDTLLVQNANP	13043	338	16	25
GAG	WMTDTLLVQ	13700	22	34	VKNWMTDTLLVQNAN	13044	337	16	25
GAG	IEVKDTKEA	13701	21	33	HQRIEVKDTKEALDK	13045	91	07	11
GAG	LQGQMVHQA	13702	21	33	VQNLQGQMVHQAISP	13046	156	15	23
GAG	MTNNPPIPV	13703	20	31	IGWMTNNPPIPVGEI	13047	268	16	25
GAG	WMTNNPPIP	13704	20	31	QIGWMTNNPPIPVGE	13048	267	16	25
GAG	IAPGQMREP	13705	19	30	AGPIAPGQMREPRGS	13049	241	19	30
GAG	VHAGPIAPG	13706	19	30	LHPVHAGPIAPGQMR	13050	236	14	22
GAG	LGPGATLEE	13707	18	28	LRALGPGATLEEMMT	13051	358	09	14
GAG	VHAGPIPPG	13708	18	28	VHPVHAGPIPPGQMR	13052	236	10	16
GAG	IPPGQMREP	13709	17	27	AGPIPPGQMREPRGS	13053	241	16	25
GAG	LSPRTLNAW	13710	17	27	HQALSPRTLNAWVKV	13054	165	10	16
GAG	YRLKHLVWA	13711	17	27	KKKYRLKHLVWASRE	13055	27	13	20
GAG	LGPAATLEE	13712	16	25	LKALGPAATLEEMMT	13056	358	16	25
GAG	LKALGPAAT	13713	16	25	KTILKALGPAATLEE	13057	355	16	25
GAG	LKDKEPPLA	13714	01	25	QEQLKDKEPPLASLR	13058	532	01	2
GAG	LSGGKLDAW	13715	16	25	ASVLSGGKLDAWEKI	13059	5	14	22
GAG	MTSNPPIPV	13716	16	25	IGWMTSNPPIPVGEI	13060	268	06	9
GAG	VKNWMTDTL	13717	16	25	TQDVKNWMTDTLLVQ	13061	334	11	17
GAG	VSILDIKQG	13718	16	25	YSPVSILDIKQGPKE	13062	301	16	25
GAG	WMTSNPPIP	13719	16	25	QIGWMTSNPPIPVGE	13063	267	06	10

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
GAG	FNTVATLYC	13720	15	23	KSLFNTVATLYCVHQ	13064	78	07	11
GAG	IPMFTALSE	13721	15	23	PEVIPMFTALSEGAT	13065	187	13	20
GAG	LASLKSLFG	13722	15	23	LYPLASLKSLFGNDP	13066	544	06	11
GAG	LERFAVNPG	13723	15	23	SRELERFAVNPGLLE	13067	39	14	22
GAG	LFNTVATLY	13724	15	23	LRSLFNTVATLYCVH	13068	77	07	11
GAG	MFTALSEGA	13725	15	23	VIPMFTALSEGATPQ	13069	189	14	22
GAG	WDRVHPVHA	13726	15	23	AAEWDRVHPVHAGPI	13070	230	12	19
GAG	IVRMYSPTS	13727	14	22	LNKIVRMYSPTSILD	13071	294	13	20
GAG	LERFALNPG	13728	14	22	SRELERFALNPGLLE	13072	39	14	22
GAG	LQEQIAWMT	13729	14	22	TSTLQEQIAWMTGNP	13073	261	05	8
GAG	VHPVHAGPI	13730	14	22	WDRVHPVHAGPIPPG	13074	233	11	17
GAG	VIPMFTALS	13731	14	22	SPEVIPMFTALSEGA	13075	186	13	20
GAG	VRMYSPTSI	13732	14	22	NKIVRMYSPTSILDI	13076	295	13	20
GAG	LGKIWPSNK	13733	13	20	ANFLGKIWPSNKGRP	13077	467	13	20
GAG	LTSLKSLFG	13734	13	20	LYPLTSLKSLFGNDP	13078	544	04	7
GAG	MYSPTSILD	13735	13	20	IVRMYSPTSILDIRQ	13079	297	12	19
GAG	YKLKHIVWA	13736	13	20	KKKYKLKHIVWASRE	13080	27	08	13
GAG	YSPTSILDI	13737	13	20	VRMYSPTSILDIRQG	13081	298	12	19
GAG	LTSLRSLFG	13738	12	19	LYPLTSLRSLFGNDP	13082	544	04	7
GAG	MMLNIVGGH	13739	12	19	DLNMMLNIVGGHQAA	13083	204	12	19
GAG	IDVKDTKEA	13740	11	17	HQRIDVKDTKEALDK	13084	91	03	5
GAG	IGWMTSNPP	13741	11	17	QEQIGWMTSNPPIPV	13085	265	09	14
GAG	IPVGDIYKR	13742	11	17	NPPIPVGDIYKRWII	13086	277	08	13
GAG	LYPLASLKS	13743	09	17	DKELYPLASLKSLFG	13087	541	06	10
GAG	VHQALSPRT	13744	11	17	GQMVHQALSPRTLNA	13088	161	07	11
GAG	VNPGLLETS	13745	11	17	RFAVNPGLLETSEGC	13089	45	11	17
GAG	YPLASLKSL	13746	08	17	KELYPLASLKSLFGN	13090	542	06	9
GAG	FLQNRPEPT	13747	10	16	PGNFLQNRPEPTAPP	13091	483	10	16
GAG	IMMQKSNFK	13748	10	16	AAAIMMQKSNFKGPR	13092	405	01	25
GAG	LAEAMSQVQ	13749	10	16	ARVLAEAMSQVQQSN	13093	384	02	3
GAG	LGKIWPSSK	13750	10	16	ANFLGKIWPSSKGRP	13094	467	10	16
GAG	LNPGLLETA	13751	10	16	RFALNPGLLETAEGC	13095	45	08	13
GAG	YPLASLRSL	13752	07	15	KELYPLASLRSLFGN	13096	542	04	6
NEF	WQNYTPGPG	13753	52	83	FPDWQNYTPGPGIRY	13097	200	15	23
NEF	VRPQVPLRP	13754	48	75	GFPVRPQVPLRPMTY	13098	93	36	56
NEF	VPLRPMTYK	13755	46	73	RPQVPLRPMTYKGAF	13099	98	07	11
NEF	LTFGWCFKL	13756	39	61	RYPLTFGWCFKLVPV	13100	216	15	24
NEF	ILDLWVYHT	13757	34	53	RQEILDLWVYHTQGY	13101	182	12	19
NEF	WCFKLVPVD	13758	26	41	TFGWCFKLVPVDPRE	13102	222	07	11
NEF	LWVYHTQGY	13759	21	33	ILDLWVYHTQGYFPD	13103	186	21	33
NEF	WSKSSIVGW	13760	20	31	GGKWSKSSIVGWPAI	13104	2	05	8
NEF	ILDLWVYNT	13761	19	30	RQDILDLWVYNTQGY	13105	182	05	8
NEF	LLHPMSQHG	13762	17	27	NNCLLHPMSQHGMDD	13106	254	06	9
NEF	LLHPICQHG	13763	16	25	NNSLLHPICQHGMED	13107	254	04	6
NEF	IRYPLTFGW	13764	13	20	GPGIRYPLTFGWCFK	13108	210	06	9
NEF	ITSSNTAAT	13765	13	20	HGAITSSNTAATNAD	13109	61	10	16
NEF	LEKHGAITS	13766	13	20	SRDLEKHGAITSSNT	13110	50	13	20
NEF	LWVYHTQGF	13767	13	20	ILDLWVYHTQGFFPD	13111	186	13	20
NEF	MTYKGAFDL	13768	12	19	LRPMTYKGAFDLSFF	13112	103	06	9
NEF	LVPVDPREV	13769	11	17	CFKLVPVDPREVEEA	13113	226	08	13

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
NEF	VGWPAIRER	13770	10	17	SSIVGWPAIRERMRR	13114	8	03	5
NEF	WCFKLVPVE	13771	11	17	TFGWCFKLVPVEPEK	13115	222	04	6
NEF	FDSRLAFHH	13772	10	16	EWRFDSRLAFHHVAR	13116	307	02	3
NEF	FKLVPVDPR	13773	10	16	GWCFKLVPVDPREVE	13117	224	10	16
NEF	VPLRPMTFK	13774	10	16	RPQVPLRPMTFKGAF	13118	98	04	6
POL	LLDTGADDT	13775	63	98	KEALLDTGADDTVLE	13119	107	37	58
POL	WMGYELHPD	13776	63	98	PFLWMGYELHPDKWT	13120	415	60	94
POL	YQYNVLPQG	13777	63	98	GIRYQYNVLPQGWKG	13121	330	52	81
POL	FRKYTAFTI	13778	61	97	DKDFRKYTAFTIPSI	13122	310	10	16
POL	WTVNDIQKL	13779	62	97	KDSWTVNDIQKLVGK	13123	438	43	67
POL	LDCTHLEGK	13780	61	95	IWQLDCTHLEGKIIL	13124	812	29	45
POL	LDVGDAYFS	13781	61	95	VTVLDVGDAYFSVPL	13125	295	50	78
POL	MDDLYVGSD	13782	61	95	YQYMDDLYVGSDLEI	13126	370	57	89
POL	VIPAETGQE	13783	61	95	EAEVIPAETGQETAY	13127	837	57	90
POL	WKGEGAVVI	13784	61	95	KLLWKGEGAVVIQDN	13128	992	53	83
POL	WQLDCTHLE	13785	61	95	PGIWQLDCTHLEGKI	13129	810	32	50
POL	VDFRELNKR	13786	60	94	RKLVDFRELNKRTQD	13130	261	57	89
POL	WKPKMIGGI	13787	60	94	PGKWKPKMIGGIGGF	13131	126	39	61
POL	IWQLDCTHL	13788	59	92	SPGIWQLDCTHLEGK	13132	809	56	88
POL	VAVHVASGY	13789	59	92	IILVAVHVASGYIEA	13133	824	26	41
POL	WKGSPAIFQ	13790	59	92	PQGWKGSPAIFQSSM	13134	339	42	66
POL	IGGYSAGER	13791	58	91	KGGIGGYSAGERIID	13135	940	37	59
POL	YALGIIQAQ	13792	58	91	DSQYALGIIQAQPDK	13136	690	39	61
POL	FWEVQLGIP	13793	57	89	TQDFWEVQLGIPHPA	13137	273	52	81
POL	IKKKDSTKW	13794	57	89	VFAIKKKDSTKWRKL	13138	249	36	56
POL	LGIIQAQPD	13795	57	89	QYALGIIQAQPDKSE	13139	692	39	61
POL	LGIPHPAGL	13796	56	89	EVQLGIPHPAGLKKK	13140	278	51	80
POL	VNTPPLVKL	13797	57	89	WEFVNTPPLVKLWYQ	13141	606	50	79
POL	VTVLDVGDA	13798	57	89	KKSVTVLDVGDAYFS	13142	292	49	77
POL	FPISPIETV	13799	56	88	TLNFPISPIETVPVK	13143	183	52	83
POL	ISPIETVPV	13800	56	88	NFPISPIETVPVKLK	13144	185	52	81
POL	FVNTPPLVK	13801	54	86	EWEFVNTPPLVKLWY	13145	605	50	78
POL	LNFPISPIE	13802	55	86	GCTLNFPISPIETVP	13146	181	53	83
POL	WEFVNTPPL	13803	54	86	IPEWEFVNTPPLVKL	13147	603	49	77
POL	IQNFRVYYR	13804	52	84	ITKIQNFRVYYRDSR	13148	969	32	51
POL	LVGPTPVNI	13805	54	84	GTVLVGPTPVNIIGR	13149	160	51	80
POL	VQLGIPHPA	13806	54	84	FWEVQLGIPHPAGLK	13150	276	53	83
POL	WQATWIPEW	13807	54	84	TEYWQATWIPEWEFV	13151	595	19	30
POL	IETVPVKLK	13808	53	83	ISPIETVPVKLKPGM	13152	188	51	80
POL	IGTVLVGPT	13809	53	83	KKAIGTVLVGPTPVN	13153	156	22	34
POL	LVAVHVASG	13810	53	83	KIILVAVHVASGYIE	13154	823	26	41
POL	VLVGPTPVN	13811	53	83	IGTVLVGPTPVNIIG	13155	159	45	70
POL	YIEAEVIPA	13812	53	83	ASGYIEAEVIPAETG	13156	832	52	81
POL	YVGSDLEIG	13813	53	83	DDLYVGSDLEIGQHR	13157	374	52	81
POL	MDGPKVKQW	13814	52	81	KPGMDGPKVKQWPLT	13158	199	47	73
POL	VASGYIEAE	13815	52	81	AVHVASGYIEAEVIP	13159	828	52	81
POL	VGPTPVNII	13816	52	81	TVLVGPTPVNIIGRN	13160	161	51	80
POL	VKQWPLTEE	13817	52	81	GPKVKQWPLTEEKIK	13161	205	45	70
POL	VYYRDSRDP	13818	52	81	NFRVYYRDSRDPIWK	13162	974	29	45
POL	WGFTTPDKK	13819	52	81	LLRWGFTTPDKKHQK	13163	398	23	36

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	VIYQYMDDL	13820	51	80	PEIVIYQYMDDLYVG	13164	365	23	36
POL	LKKKKSVTV	13821	49	78	PAGLKKKKSVTVLDV	13165	286	46	72
POL	VPRRKAKII	13822	50	78	IKVVPRRKAKIIRDY	13166	1010	41	64
POL	FPQITLWQR	13823	49	77	SFSFPQITLWQRPLV	13167	84	09	14
POL	VIWGKTPKF	13824	47	73	ESIVIWGKTPKFRLP	13168	570	23	37
POL	YVDGAANRE	13825	46	72	ETFYVDGAANRETKL	13169	630	24	38
POL	FKNLKTGKY	13826	45	70	QEPFKNLKTGKYAKM	13170	535	15	23
POL	IQTKELQKQ	13827	45	70	ATDIQTKELQKQITK	13171	957	24	38
POL	YGKQMAGDD	13828	45	70	IRDYGKQMAGDDCVA	13172	1021	41	64
POL	WRAMASDFN	13829	43	67	HSNWRAMASDFNLPP	13173	768	31	48
POL	ISKIGPENP	13830	42	66	EGKISKIGPENPYNT	13174	233	40	63
POL	LTQIGCTLN	13831	41	64	RNLLTQIGCTLNFPI	13175	174	21	33
POL	IIQAQPDKS	13832	40	63	ALGIIQAQPDKSESE	13176	694	38	59
POL	LPEKDSWTV	13833	40	63	PIVLPEKDSWTVNDI	13177	432	13	20
POL	FQSSMTKIL	13834	38	59	PAIFQSSMTKILEPF	13178	346	32	50
POL	FTIPSINNE	13835	38	59	YTAFTIPSINNETPG	13179	316	36	56
POL	IFQSSMTKI	13836	38	59	SPAIFQSSMTKILEP	13180	345	33	52
POL	IIEQLIKKE	13837	37	58	VSQIIEQLIKKEKVY	13181	710	19	30
POL	LSWVPAHKG	13838	37	58	KVYLSWVPAHKGIGG	13182	722	23	37
POL	YLSWVPAHK	13839	37	58	EKVYLSWVPAHKGIG	13183	721	15	24
POL	YTAFTIPSI	13840	37	58	FRKYTAFTIPSINNE	13184	313	37	59
POL	IIATDIQTK	13841	35	55	IIDIIATDIQTKELQ	13185	952	22	34
POL	IWKGPAKLL	13842	35	55	RDPIWKGPAKLLWKG	13186	983	34	53
POL	LQKQITKIQ	13843	35	55	TKELQKQITKIQNFR	13187	962	29	46
POL	LKEALLDTG	13844	34	53	GGQLKEALLDTGADD	13188	103	31	48
POL	VYLSWVPAH	13845	33	52	KEKVYLSWVPAHKGI	13189	720	15	23
POL	FILKLAGRW	13846	32	50	TAYFILKLAGRWPVK	13190	849	27	42
POL	LEGKIILVA	13847	31	48	CTHLEGKIILVAVHV	13191	817	30	47
POL	YFILKLAGR	13848	31	48	ETAYFILKLAGRWPV	13192	848	30	47
POL	IILVAVHVA	13849	30	47	EGKIILVAVHVASGY	13193	821	30	47
POL	IWGKTPKFR	13850	30	47	SIVIWGKTPKFRLPI	13194	571	22	34
POL	LAGRWPVKV	13851	30	47	ILKLAGRWPVKVIHT	13195	853	19	30
POL	VVAKEIVAS	13852	30	47	LPPVVAKEIVASCDK	13196	780	21	33
POL	IDIIATDIQ	13853	29	45	ERIIDIIATDIQTKE	13197	950	22	34
POL	IIDIIATDI	13854	29	45	GERIIDIIATDIQTK	13198	949	23	36
POL	IIGRNMLTQ	13855	29	45	PVNIIGRNMLTQIGC	13199	168	11	17
POL	IKVKQLCKL	13856	29	45	YAGIKVKQLCKLLRG	13200	460	18	28
POL	VDKLVSSGI	13857	29	45	NEQVDKLVSSGIRKV	13201	737	26	41
POL	IVGAETFYV	13858	28	44	KEPIVGAETFYVDGA	13202	623	16	25
POL	LPPVVAKEI	13859	28	44	DFNLPPVVAKEIVAS	13203	777	26	41
POL	WTVQPIQLP	13860	28	44	PDKWTVQPIQLPEKD	13204	425	13	20
POL	FNLPPVVAK	13861	27	42	ASDFNLPPVVAKEIV	13205	775	25	39
POL	FTSAAVKAA	13862	27	42	GSNFTSAAVKAACWW	13206	870	25	39
POL	LALQDSGLE	13863	27	42	AIHLALQDSGLEVNI	13207	673	15	23
POL	LPPIVAKEI	13864	27	42	DFNLPPIVAKEIVAS	13208	777	20	31
POL	LQDSGLEVN	13865	27	42	HLALQDSGLEVNIVT	13209	675	13	20
POL	FNLPPIVAK	13866	26	41	ASDFNLPPIVAKEIV	13210	775	21	33
POL	IGQHRAKIE	13867	26	41	DLEIGQHRAKIEELR	13211	381	23	36
POL	IIGRNLLTQ	13868	26	41	PVNIIGRNLLTQIGC	13212	168	21	33
POL	LEVNIVTDS	13869	26	41	DSGLEVNIVTDSQYA	13213	680	26	41

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	LRGAKALTD	13870	26	41	CKLLRGAKALTDIVP	13214	469	12	19
POL	LVSSGIRKV	13871	26	41	VDKLVSSGIRKVLFL	13215	740	25	39
POL	FLLKLAGRW	13872	25	39	TAYFLLKLAGRWPVK	13216	849	19	30
POL	LALQDSGSE	13873	25	39	AIHLALQDSGSEVNI	13217	673	08	13
POL	LQDSGSEVN	13874	25	39	HLALQDSGSEVNIVT	13218	675	08	13
POL	VKVIHTDNG	13875	25	39	RWPVKVIHTDNGSNF	13219	859	21	33
POL	WPVKVIHTD	13876	25	39	AGRWPVKVIHTDNGS	13220	857	20	31
POL	YFLLKLAGR	13877	25	39	ETAYFLLKLAGRWPV	13221	848	24	38
POL	ICGKKAIGT	13878	24	38	LIEICGKKAIGTVLV	13222	150	12	19
POL	IVAKEIVAS	13879	24	38	LPPIVAKEIVASCDK	13223	780	22	34
POL	LRWGFTTPD	13880	24	38	QHLLRWGFTTPDKKH	13224	396	12	19
POL	LEGKVILVA	13881	23	36	CTHLEGKVILVAVHV	13225	817	23	36
POL	LKWGFTTPD	13882	23	36	EHLLKWGFTTPDKKH	13226	396	13	20
POL	VILVAVHVA	13883	23	36	EGKVILVAVHVASGY	13227	821	21	33
POL	LAWVPAHKG	13884	22	34	KVYLAWVPAHKGIGG	13228	722	20	32
POL	YDQILIEIC	13885	22	34	VRQYDQILIEICGKK	13229	143	08	13
POL	YLAWVPAHK	13886	22	34	EKVYLAWVPAHKGIG	13230	721	20	32
POL	IGQHRTKIE	13887	21	33	DLEIGQHRTKIEELR	13231	381	19	30
POL	IGRNLLTQI	13888	21	33	VNIIGRNLLTQIGCT	13232	169	21	33
POL	LWQRPLVTI	13889	21	33	QITLWQRPLVTIKIG	13233	89	11	17
POL	VSLTETTNQ	13890	21	33	QKVVSLTETTNQKTE	13234	656	10	16
POL	VYLAWVPAH	13891	21	33	KEKVYLAWVPAHKGI	13235	720	20	31
POL	ICGHKAIGT	13892	20	31	LIEICGHKAIGTVLV	13236	150	10	16
POL	LRGTKALTE	13893	19	30	CKLLRGTKALTEVIP	13237	469	11	17
POL	LVNQIIEQL	13894	19	30	ESELVNQIIEQLIKK	13238	706	13	20
POL	LVSQIIEQL	13895	19	30	ESELVSQIIEQLIKK	13239	706	18	28
POL	YFSVPLDKD	13896	18	29	GDAYFSVPLDKDFRK	13240	301	18	28
POL	IGRNMLTQI	13897	18	28	VNIIGRNMLTQIGCT	13241	169	12	19
POL	IKVRQLCKL	13898	18	28	YPGIKVRQLCKLLRG	13242	460	13	20
POL	LWKGPAKLL	13899	18	28	RDPLWKGPAKLLWKG	13243	983	13	20
POL	LWQRPLVTV	13900	18	28	QITLWQRPLVTVKIG	13244	89	09	14
POL	YAGIKVKQL	13901	18	28	SQIYAGIKVKQLCKL	13245	457	18	28
POL	IWGKTPKFK	13902	17	27	SIVIWGKTPKFKLPI	13246	571	17	27
POL	LREHLLKWG	13903	17	27	IEELREHLLKWGFTT	13247	391	12	19
POL	VQPIQLPEK	13904	17	27	KWTVQPIQLPEKDSW	13248	427	13	20
POL	WQRPLVTIK	13905	17	27	ITLWQRPLVTIKIGG	13249	90	11	17
POL	IIQAQPDRS	13906	16	25	ALGIIQAQPDRSESE	13250	694	12	19
POL	LQAIHLALQ	13907	16	25	KTELQAIHLALQDSG	13251	668	15	23
POL	LVEICTEME	13908	15	24	IKALVEICTEMEKEG	13252	218	15	23
POL	LRQHLLRWG	13909	15	23	IEELRQHLLRWGFTT	13253	391	12	19
POL	LTQLGCTLN	13910	15	23	RNMLTQLGCTLNFPI	13254	174	10	16
POL	LVSAGIRKV	13911	15	23	VDKLVSAGIRKVLFL	13255	740	14	22
POL	VDKLVSAGI	13912	15	23	NEQVDKLVSAGIRKV	13256	737	14	22
POL	YPGIKVRQL	13913	15	23	SQIYPGIKVRQLCKL	13257	457	12	19
POL	FRKQNPDIV	13914	14	22	LEPFRKQNPDIVIYQ	13258	357	14	22
POL	FSFPQITLW	13915	14	22	TVSFSFPQITLWQRP	13259	77	05	10
POL	FTSTTVKAA	13916	14	22	GSNFTSTTVKAACWW	13260	870	11	17
POL	IIASDIQTK	13917	14	22	IIDIIASDIQTKELQ	13261	952	11	17
POL	LAGRWPVKT	13918	14	22	LLKLAGRWPVKTIHT	13262	853	09	14
POL	VQKIATESI	13919	14	22	TEAVQKIATESIVIW	13263	561	10	16

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	FTIPSTNNE	13920	13	20	YTAFTIPSTNNETPG	13264	316	13	20
POL	LEDINLPGK	13921	13	20	DTVLEDINLPGKWKP	13265	117	13	20
POL	LTDIVPLTE	13922	13	20	AKALTDIVPLTEEAE	13266	475	08	13
POL	LVTIKIGGQ	13923	13	20	QRPLVTIKIGGQLKE	13267	94	13	20
POL	MRGAHTNDV	13924	13	20	YARMRGAHTNDVKQL	13268	546	12	19
POL	VKTIHTDNG	13925	13	20	RWPVKTIHTDNGSNF	13269	859	09	14
POL	VQPIVLPEK	13926	13	20	KWTVQPIVLPEKDSW	13270	427	12	19
POL	WPVKTIHTD	13927	13	20	AGRWPVKTIHTDNGS	13271	857	09	14
POL	WQRPLVTVK	13928	13	20	ITLWQRPLVTVKIGG	13272	90	09	14
POL	WTVQPIVLP	13929	13	20	PDKWTVQPIVLPEKD	13273	425	12	19
POL	YTAFTIPST	13930	13	20	FRKYTAFTIPSTNNE	13274	313	13	21
POL	IDIIASDIQ	13931	12	19	ERIIDIIASDIQTKE	13275	950	11	17
POL	IIDIIASDI	13932	12	19	GERIIDIIASDIQTK	13276	949	11	17
POL	IVDIIATDI	13933	12	19	GERIVDIIATDIQTK	13277	949	10	16
POL	LEEINLPGK	13934	12	19	DTVLEEINLPGKWKP	13278	117	11	17
POL	LQAIYLALQ	13935	12	19	KTELQAIYLALQDSG	13279	668	11	17
POL	LQKQIIKIQ	13936	12	19	TKELQKQIIKIQNFR	13280	962	09	14
POL	VDIIATDIQ	13937	12	19	ERIVDIIATDIQTKE	13281	950	10	16
POL	YDQIPIEIC	13938	12	19	VRQYDQIPIEICGKK	13282	143	05	8
POL	FNFPQITLW	13939	11	17	VPTFNFPQITLWQRP	13283	79	01	17
POL	IGRNMLTQL	13940	11	17	VNIIGRNMLTQLGCT	13284	169	10	16
POL	ISRIGPENP	13941	11	17	EGKISRIGPENPYNT	13285	233	10	16
POL	LTEVIPLTE	13942	11	17	TKALTEVIPLTEEAE	13286	475	10	16
POL	MESIVIWGK	13943	11	17	KIAMESIVIWGKTPK	13287	566	07	11
POL	VPRRKVKII	13944	11	17	IKVVPRRKVKIIRDY	13288	1010	08	13
POL	VSFSFPQIT	13945	08	17	QGTVSFSFPQITLWQ	13289	75	05	8
POL	WYQLETEPI	13946	11	17	VKLWYQLETEPIVGA	13290	615	04	6
POL	YPGIKVKQL	13947	11	17	SQIYPGIKVKQLCKL	13291	457	09	14
POL	FPQGEAREF	13948	10	16	NLAFPQGEAREFPPE	13292	5	05	8
POL	LIEALLDTG	13949	10	16	GGQLIEALLDTGADD	13293	103	09	14
POL	VSLTDTTNQ	13950	10	16	QKVVSLTDTTNQKTE	13294	656	09	14
POL	WETWWTDYW	13951	10	16	KETWETWWTDYWQAT	13295	587	09	14
POL	YAKMRTAHT	13952	10	16	TGKYAKMRTAHTNDV	13296	543	09	14
POL	YKNLKTGKY	13953	10	16	QEPYKNLKTGKYARM	13297	535	03	5
REV	LQLPPLERL	13954	36	56	PVPLQLPPLERLTLD	13298	74	13	20
REV	VPLQLPPLE	13955	36	56	AEPVPLQLPPLERLT	13299	72	10	16
REV	LYQSNPPPS	13956	18	28	IKFLYQSNPPPSPEG	13300	21	04	6
REV	VRIIKILYQ	13957	16	25	LKAVRIIKILYQSNP	13301	13	06	9
REV	YQSNPPPSP	13958	12	19	KFLYQSNPPPSPEGT	13302	22	05	8
REV	LQLPPIERL	13959	11	17	PVPLQLPPIERLRLD	13303	74	04	6
REV	VPLQLPPIE	13960	11	17	AEPVPLQLPPIERLR	13304	72	04	6
TAT	WNHPGSQPK	13961	15	23	LEPWNHPGSQPKTAC	13305	11	11	17
TAT	FLNKGLGIS	13962	14	22	QVCFLNKGLGISYGR	13306	38	04	6
TAT	WKHPGSQPK	13963	13	20	LEPWKHPGSQPKTAC	13307	11	11	17
TAT	YCKKCCFHC	13964	11	17	NNCYCKKCCFHCQVC	13308	26	04	6
TAT	YCKKCCYHC	13965	11	17	TNCYCKKCCYHCQVC	13309	26	02	3
TAT	WNHPGSQPT	13966	10	16	LEPWNHPGSQPTTAC	13310	11	07	11
VIF	MIVWQVDRM	13967	46	72	WQVMIVWQVDRMRIR	13311	5	28	44
VIF	WQVMIVWQV	13968	43	67	ENRWQVMIVWQVDRM	13312	2	41	64
VIF	WQVDRMRIR	13969	34	53	MIVWQVDRMRIRTWK	13313	8	14	22

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
VIF	LQYLALTAL	13970	33	52	VGSLQYLALTALIKP	13314	147	14	22
VIF	LGHGVSIEW	13971	31	48	DWHLGHGVSIEWRLR	13315	81	11	17
VIF	VDRMRIRTW	13972	31	48	VWQVDRMRIRTWNSL	13316	10	15	23
VIF	YFDCFSESA	13973	28	44	HLYYFDCFSESAIRN	13317	113	08	13
VIF	YWGLHTGER	13974	28	44	ITTYWGLHTGERDWH	13318	68	14	22
VIF	IRTWNSLVK	13975	27	42	RMRIRTWNSLVKHHM	13319	15	12	19
VIF	LGQGVSIEW	13976	26	41	DWHLGQGVSIEWRKK	13320	81	07	11
VIF	LVKHHMYVS	13977	21	33	WNSLVKHHMYVSKKA	13321	21	07	11
VIF	IPLGEARLV	13978	19	30	EVHIPLGEARLVVRT	13322	54	05	8
VIF	LVKHHMYIS	13979	19	30	WKSLVKHHMYISGKA	13323	21	05	8
VIF	YLALTALIK	13980	16	25	SLQYLALTALIKPKK	13324	149	11	17
VIF	IRTWKSLVK	13981	15	23	RMRIRTWKSLVKHHM	13325	15	14	22
VIF	LADQLIHLY	13982	15	23	DPDLADQLIHLYYFD	13326	104	07	11
VIF	LALTALIKP	13983	15	23	LQYLALTALIKPKKI	13327	150	08	13
VIF	VDPGLADQL	13984	15	23	STQVDPGLADQLIHL	13328	100	04	6
VIF	LYYFDCFSE	13985	14	22	LIHLYYFDCFSESAI	13329	111	14	22
VIF	FSESAIRKA	13986	13	20	FDCFSESAIRKAILG	13330	117	10	16
VIF	LADQLIHMH	13987	13	20	EPGLADQLIHMHYFD	13331	104	08	13
VIF	WQVDRMKIR	13988	13	20	LIVWQVDRMKIRTWN	13332	8	09	14
VIF	FSDSAIRKA	13989	12	19	FDCFSDSAIRKAILG	13333	117	05	8
VIF	FSESAIRNA	13990	12	19	FDCFSESAIRNAILG	13334	117	12	19
VIF	IVSPRCEYQ	13991	12	19	LGHIVSPRCEYQAGH	13335	130	06	9
VIF	LQYLALAAL	13992	12	19	VGSLQYLALAALITP	13336	147	04	6
VIF	VDRMKIRTW	13993	12	19	VWQVDRMKIRTWNSL	13337	10	12	19
VIF	YWGLQTGER	13994	12	19	IKTYWGLQTGERDWH	13338	68	08	13
VIF	IPLGDARLV	13995	11	17	EVHIPLGDARLVITT	13339	54	06	9
VIF	LQYLALKAL	13996	11	17	VGSLQYLALKALVTP	13340	147	08	13
VIF	WQVDRMRIN	13997	11	17	MIVWQVDRMRINTWK	13341	8	08	13
VIF	IKPKKIKPP	13998	10	16	TALIKPKKIKPPLPS	13342	156	08	13
VIF	VDRMRINTW	13999	10	16	VWQVDRMRINTWKSL	13343	10	09	14
VPR	IGCQHSRIG	14000	46	72	HFRIGCQHSRIGITR	13344	71	08	13
VPR	WTLELLEEL	14001	42	69	YNEWTLELLEELKSE	13345	15	12	19
VPR	ILQQLLFIH	14002	37	58	IIRILQQLLFIHFRI	13346	60	31	48
VPR	FIHFRIGCQ	14003	30	47	QLLFIHFRIGCQHSR	13347	66	29	45
VPR	YNEWTLELL	14004	30	47	REPYNEWTLELLEEL	13348	12	27	42
VPR	FPRPWLHGL	14005	24	38	VRHFPRPWLHGLGQH	13349	31	12	19
VPR	WEGVEAIIR	14006	18	28	GDTWEGVEAIIRILQ	13350	51	14	22
VPR	LEELKSEAV	14007	16	25	LELLEELKSEAVRHF	13351	20	15	23
VPR	WAGVEAIIR	14008	16	25	GDTWAGVEAIIRILQ	13352	51	15	23
VPR	YGDTWAGVE	14009	16	25	YETYGDTWAGVEAII	13353	47	16	25
VPR	IGCRHSRIG	14010	12	19	HFRIGCRHSRIGITR	13354	71	03	5
VPR	FIHFRIGCR	14011	11	17	QLLFIHFRIGCRHSR	13355	66	11	17
VPR	FVHFRIGCQ	14012	11	17	QLLFVHFRIGCQHSR	13356	66	10	16
VPR	YGDTWTGVE	14013	11	17	YETYGDTWTGVEAII	13357	47	04	6
VPR	FPRIWLHSL	14014	10	16	VRHFPRIWLHSLGQH	13358	31	05	8
VPR	WALELLEEL	14015	09	15	YNEWALELLEELKNE	13359	15	03	5
VPU	LVTLLSSSK	14016	01	50	EEWLVTLLSSSKLDQ	13360	87	01	2
VPU	VTLLSSSKL	14017	01	50	EWLVTLLSSSKLDQG	13361	89	01	2
VPU	IIAIVVWTI	14018	23	36	VVAIIAIVVWTIVFI	13362	20	02	3
VPU	VDYRIVIVA	14019	01	33	LAKVDYRIVIVAFIV	13363	5	01	25

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
VPU	LRQRKIDRL	14020	17	27	RKILRQRKIDRLIDR	13364	44	11	17
VPU	IVVWTIVFI	14021	15	23	IIAIVVWTIVFIEYR	13365	27	07	11
VPU	VVWTIVFIE	14022	14	22	IAIVVWTIVFIEYRK	13366	28	06	9
VPU	IEYRKILRQ	14023	13	21	IVFIEYRKILRQRKI	13367	36	07	11
VPU	ILAIVALVV	14024	11	17	SLYILAIVALVVAII	13368	3	01	2
VPU	WTIVFIEYR	14025	10	16	IVVWTIVFIEYRKIL	13369	30	05	8
VPU	LAIVALVVA	14026	09	15	LQILAIVALVVAGII	13370	4	02	3

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VSTQLLLNG	13520	KPVVSTQLLLNGSLA	12864								
VVSTQLLLN	13521	IKPVVSTQLLLNGSL	12865								
LTVWGIKQL	13522	LLQLTVWGIKQLQAR	12866	0.0840		0.0096		0.0190		0.0750	
LLSGIVQQQ	13523	ARQLLSGIVQQQSNL	12867								
WATHACVPT	13524	HNVWATHACVPTDPN	12868								
LGAAGSTMG	13525	LGFLGAAGSTMGAAS	12869								
VRQGYSPLS	13526	VNRVRQGYSPLSFQT	12870	0.0032		-0.0014		0.0230		-0.0010	
LLLNGSLAE	13527	STQLLLNGSLAEEEV	12871								
VKLTPLCVT	13528	KPCVKLTPLCVTLNC	12872								
LRAIEAQQH	13529	NNLLRAIEAQQHLLQ	12873	0.0280				0.0150			
VSTVQCTHG	13530	CKNVSTVQCTHGIKP	12874								
LGIWGCSGK	13531	QQLLGIWGCSGKLIC	12875								
LWDQSLKPC	13532	IISLWDQSLKPCVKL	12876	0.0057		0.0061		0.0096		0.0059	
LGFLGAAGS	13533	AVFLGFLGAAGSTMG	12877								
VWATHACVP	13534	VHNVWATHACVPTDP	12878								
WGIKQLQAR	13535	LTVWGIKQLQARVLA	12879								
LWYIKIFIM	13536	TNWLWYIKIFIMIVG	12880								
FCASDAKAY	13537	TTLFCASDAKAYDTE	12881								
IVGGLIGLR	13538	FIMIVGGLIGLRIVF	12882								
IFIMIVGGL	13539	YIKIFIMIVGGLIGL	12883								
VYYGVPVWK	13540	WVTVYYGVPVWKEAT	12884	0.0790	6.1000	0.0700	0.0043	0.0180	8.2000	-0.0010	0.0098
IKQLQARVL	13541	VWGIKQLQARVLAVE	12885								
IKIFIMIVG	13542	LWYIKIFIMIVGGLI	12886								
MGAASITLT	13543	GSTMGAASITLTVQA	12887								
YIKIFIMIV	13544	WLWYIKIFIMIVGGL	12888								
ITGLLLTRD	13545	SSNITGLLLTRDGGK	12889								
IPIHYCAPA	13546	FEPIPIHYCAPAGFA	12890								
MIVGGLIGL	13547	IFIMIVGGLIGLRIV	12891								
VQARQLLSG	13548	TLTVQARQLLSGIVQ	12892								
FEPIPIHYC	13549	KVSFEPIPIHYCAPA	12893								
LRSLCLFSY	13550	WDDLRSLCLFSYHRL	12894								
MWKNNMVEQ	13551	NFNMWKNNMVEQMHE	12895								
VHNVWATHA	13552	DTEVHNVWATHACVP	12896								
WKNNMVEQM	13553	FNMWKNNMVEQMHED	12897								
YYGVPVWKE	13554	VTVYYGVPVWKEATT	12898	0.0087		0.0270		0.0071		0.0021	
LLQLTVWGI	13555	QQHLLQLTVWGIKQL	12899	1.1000	0.7500	0.0580	-0.0043	0.0330	0.2700	0.0036	0.4900
IEPLGVAPT	13556	VVKIEPLGVAPTKAK	12900								
IKPVVSTQL	13557	THGIKPVVSTQLLLN	12901								
LQARVLAVE	13558	IKQLQARVLAVERYL	12902								
WDDLRSLCL	13559	ALAWDDLRSLCLFSY	12903								
IINIHTPHR	13560	SRPIINIHTPHREKR	12904								
INIHTPHRE	13561	RPIINIHTPHREKRA	12905								
ITQACPKVS	13562	TSVITQACPKVSFEP	12906								
IVQQQSNLL	13563	LSGIVQQQSNLLRAI	12907								
LGNNSTNST	13564	NKTLGNNSTNSTLGN	12908								
VISTRTHRE	13565	ARPVISTRTHREKRA	12909								
WRWGTLFLG	13566	QNLWRWGTLFLGMLM	12910								
WRWGTMLLG	13567	QHLWRWGTMLLGMLM	12911								
FAVLSIVNR	13568	RIVFAVLSIVNRVRQ	12912								
LLNGSLAEE	13569	TQLLLNGSLAEEEVV	12913								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VSTQLLLNG	13520	KPVVSTQLLLNGSLA	12864					
VVSTQLLLN	13521	IKPVVSTQLLLNGSL	12865					
LTVWGIKQL	13522	LLQLTVWGIKQLQAR	12866		0.0180			
LLSGIVQQQ	13523	ARQLLSGIVQQQSNL	12867					
WATHACVPT	13524	HNVWATHACVPTDPN	12868					
LGAAGSTMG	13525	LGFLGAAGSTMGAAS	12869					
VRQGYSPLS	13526	VNRVRQGYSPLSFQT	12870		-0.0007			
LLLNGSLAE	13527	STQLLLNGSLAEEEV	12871					
VKLTPLCVT	13528	KPCVKLTPLCVTLNC	12872					
LRAIEAQQH	13529	NNLLRAIEAQQHLLQ	12873		0.0150			
VSTVQCTHG	13530	CKNVSTVQCTHGIKP	12874					
LGIWGCSGK	13531	QQLLGIWGCSGKLIC	12875					
LWDQSLKPC	13532	IISLWDQSLKPCVKL	12876		0.0012			
LGFLGAAGS	13533	AVFLGFLGAAGSTMG	12877					
VWATHACVP	13534	VHNVWATHACVPTDP	12878					
WGIKQLQAR	13535	LTVWGIKQLQARVLA	12879					
LWYIKIFIM	13536	TNWLWYIKIFIMIVG	12880					
FCASDAKAY	13537	TTLFCASDAKAYDTE	12881					
IVGGLIGLR	13538	FIMIVGGLIGLRIVF	12882					
IFIMIVGGL	13539	YIKIFIMIVGGLIGL	12883					
VYYGVPVWK	13540	WVTVYYGVPVWKEAT	12884	-0.0004	0.0310	0.0049	0.4600	
IKQLQARVL	13541	VWGIKQLQARVLAVE	12885					
IKIFIMIVG	13542	LWYIKIFIMIVGGLI	12886					
MGAASITLT	13543	GSTMGAASITLTVQA	12887					
YIKIFIMIV	13544	WLWYIKIFIMIVGGL	12888					
ITGLLLTRD	13545	SSNITGLLLTRDGGK	12889					
IPIHYCAPA	13546	FEPIPIHYCAPAGFA	12890					
MIVGGLIGL	13547	IFIMIVGGLIGLRIV	12891					
VQARQLLSG	13548	TLTVQARQLLSGIVQ	12892					
FEPIPIHYC	13549	KVSFEPIPIHYCAPA	12893					
LRSLCLFSY	13550	WDDLRSLCLFSYHRL	12894					
MWKNNMVEQ	13551	NFNMWKNNMVEQMHE	12895					
VHNVWATHA	13552	DTEVHNVWATHACVP	12896					
WKNNMVEQM	13553	FNMWKNNMVEQMHED	12897					
YYGVPVWKE	13554	VTVYYGVPVWKEATT	12898		0.0160			
LLQLTVWGI	13555	QQHLLQLTVWGIKQL	12899	0.0180	0.3900	0.0210	0.5100	
IEPLGVAPT	13556	VVKIEPLGVAPTKAK	12900					
IKPVVSTQL	13557	THGIKPVVSTQLLLN	12901					
LQARVLAVE	13558	IKQLQARVLAVERYL	12902					
WDDLRSLCL	13559	ALAWDDLRSLCLFSY	12903					
IINIHTPHR	13560	SRPIINIHTPHREKR	12904					
INIHTPHRE	13561	RPIINIHTPHREKRA	12905					
ITQACPKVS	13562	TSVTTQACPKVSFEP	12906					
IVQQQSNLL	13563	LSGIVQQQSNLLRAI	12907					
LGNNSTNST	13564	NKTLGNNSTNSTLGN	12908					
VISTRTHRE	13565	ARPVISTRTHREKRA	12909					
WRWGTLFLG	13566	QNLWRWGTLFLGMLM	12910					
WRWGTMLLG	13567	QHLWRWGTMLLGMLM	12911					
FAVLSIVNR	13568	RIVFAVLSIVNRVRQ	12912					
LLNGSLAEE	13569	TQLLLNGSLAEEEVV	12913					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LTPLCVTLN	13570	CVKLTPLCVTLNCTD	12914								
LYKYKVVKI	13571	RSELYKYKVVKIEPL	12915	0.0066	0.0320	0.0014		0.0011	0.0190	0.0042	
VPWNSSWSN	13572	TTNVPWNSSWSNKSL	12916								
YRLINCNTS	13573	YKEYRLINCNTSAIT	12917								
IHYCAPAGF	13574	PIPIHYCAPAGFAIL	12918								
LKDQQLLGI	13575	ERYLKDQQLLGIWGC	12919								
YKYKVVKIE	13576	SELYKYKVVKIEPLG	12920								
IRPVVSTQL	13577	THGIRPVVSTQLLLN	12921								
LDKWASLWN	13578	LLALDKWASLWNWFD	12922								
LRIVFAVLS	13579	LIGLRIVFAVLSIVN	12923								
LNGSLAEEE	13580	QLLLNGSLAEEEVVI	12924								
YKVVKIEPL	13581	LYKYKVVKIEPLGVA	12925								
LKGLRLGWE	13582	RSSLKGLRLGWEGLK	12926								
FSYHRLRDL	13583	LCLFSYHRLRDLLLI	12927								
INCTRPNNN	13584	SVEINCTRPNNNTRK	12928								
VVKIEPLGV	13585	KYKVVKIEPLGVAPT	12929								
WKEATTTLF	13586	VPVWKEATTTLFCAS	12930	0.0260	-0.0002	0.0520	-0.0030	0.1100	0.0900	0.0021	-0.0045
IGLRIVFAV	13587	GGLIGLRIVFAVLSI	12931								
FFYCNTSGL	13588	GGEFFYCNTSGLFNS	12932								
FGLGALFLG	13589	RAAFGLGALFLGFLG	12933								
FYCNTSGLF	13590	GEFFYCNTSGLFNST	12934								
LIGLRIVFA	13591	VGGLIGLRIVFAVLS	12935								
VGLGAVFLG	13592	KRAVGLGAVFLGFLG	12936								
VGLGMLFLG	13593	KRAVGLGMLFLGVLS	12937								
ICTTAVPWN	13594	GKLICTTAVPWNSSW	12938								
ICTTNVPWN	13595	GKLICTTNVPWNSSW	12939								
LGVAPTKAK	13596	IEPLGVAPTKAKRRV	12940								
LICTTAVPW	13597	SGKLICTTAVPWNSS	12941								
LRDQQLLGI	13598	ERYLRDQQLLGIWGC	12942								
VFLGFLGAA	13599	LGAVFLGFLGAAGST	12943								
FSYHRLRDF	13600	LCLFSYHRLRDFILI	12944								
IPIHYCTPA	13601	FEPIPIHYCTPAGFA	12945								
IVFAVLSIV	13602	GLRIVFAVLSIVNRV	12946								
VFAVLSIVN	13603	LRIVFAVLSIVNRVR	12947								
VPWNASWSN	13604	TTAVPWNASWSNKSL	12948								
IGLRIIFAV	13605	GGLIGLRIIFAVLSI	12949								
IRQAHCNIS	13606	IGDIRQAHCNISRAK	12950								
VAPTKAKRR	13607	PLGVAPTKAKRRVVQ	12951								
FNGTGPCKN	13608	DKKFNGTGPCKNVST	12952								
IGPGQTFYA	13609	SVRIGPGQTFYATGD	12953								
IGSGQAFYV	13610	RYSIGSGQAFYVTGK	12954								
IRYLNLVNQ	13611	QTAIRYLNLVNQTEN	12955								
LIGLRIIFA	13612	VGGLIGLRIIFAVLS	12956								
LLQYWSQEL	13613	WWNLLQYWSQELKNS	12957								
LRNLCLFSY	13614	WDDLRNLCLFSYHRL	12958								
LVSGFLALA	13615	SIRLVSGFLALAWDD	12959								
VSGFLALAW	13616	IRLVSGFLALAWDDL	12960								
FDPIPIHYC	13617	KVTFDPIPIHYCTPA	12961								
IIFAVLSIV	13618	GLRIIFAVLSIVNRV	12962								
LINCNTSAI	13619	EYRLINCNTSAITQA	12963								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
		CVKLTPLCVTLNCTD	12914					
LTPLCVTLN	13570	RSELYKYKVVKIEPL	12915	0.0100	0.1800	0.1100	0.1700	
LYKYKVVKI	13571	TTNVPWNSSWSNKSL	12916					
VPWNSSWSN	13572	YKEYRLINCNTSAIT	12917					
YRLINCNTS	13573	PIPIHYCAPAGFAIL	12918					
IHYCAPAGF	13574	ERYLKDQQLLGIWGC	12919					
LKDQQLLGI	13575	SELYKYKVVKIEPLG	12920					
YKYKVVKIE	13576	THGIRPVVSTQLLLN	12921					
IRPVVSTQL	13577	LLALDKWASLWNWFD	12922					
LDKWASLWN	13578	LIGLRIVFAVLSIVN	12923					
LRIVFAVLS	13579	QLLLNGSLAEEEVVI	12924					
LNGSLAEEE	13580	LYKYKVVKIEPLGVA	12925					
YKVVKIEPL	13581	RSSLKGLRLGWEGLK	12926					
LKGLRLGWE	13582	LCLFSYHRLRDLLLI	12927					
FSYHRLRDL	13583	SVEINCTRPNNNTRK	12928					
INCTRPNNN	13584	KYKVVKIEPLGVAPT	12929					
VVKIEPLGV	13585	VPVWKEATTTLFCAS	12930	0.0004	0.0630	0.0086	0.4700	
WKEATTTLF	13586	GGLIGLRIVFAVLSI	12931					
IGLRIVFAV	13587	GGEFFYCNTSGLFNS	12932					
FFYCNTSGL	13588	RAAFGLGALFLGFLG	12933					
FGLGALFLG	13589	GEFFYCNTSGLFNST	12934					
FYCNTSGLF	13590	VGGLIGLRIVFAVLS	12935					
LIGLRIVFA	13591	KRAVGLGAVFLGFLG	12936					
VGLGAVFLG	13592	KRAVGLGMLFLGVLS	12937					
VGLGMLFLG	13593	GKLICTTAVPWNSSW	12938					
ICTTAVPWN	13594	GKLICTTNVPWNSSW	12939					
ICTTNVPWN	13595	IEPLGVAPTKAKRRV	12940					
LGVAPTKAK	13596	SGKLICTTAVPWNSS	12941					
LICTTAVPW	13597	ERYLRDQQLLGIWGC	12942					
LRDQQLLGI	13598	LGAVFLGFLGAAGST	12943					
VFLGFLGAA	13599	LCLFSYHRLRDFILI	12944					
FSYHRLRDF	13600	FEPIPIHYCTPAGFA	12945					
IPIHYCTPA	13601	GLRIVFAVLSIVNRV	12946					
IVFAVLSIV	13602	LRIVFAVLSIVNRVR	12947					
VFAVLSIVN	13603	TTAVPWNASWSNKSL	12948					
VPWNASWSN	13604	GGLIGLRIIFAVLSI	12949					
IGLRIIFAV	13605	IGDIRQAHCNISRAK	12950					
IRQAHCNIS	13606	PLGVAPTKAKRRVVQ	12951					
VAPTKAKRR	13607	DKKFNGTGPCKNVST	12952					
FNGTGPCKN	13608	SVRIGPGQTFYATGD	12953					
IGPGQTFYA	13609	RYSIGSGQAFYVTGK	12954					
IGSGQAFYV	13610	QTAIRYLNLVNQTEN	12955					
IRYLNLVNQ	13611	VGGLIGLRIIFAVLS	12956					
LIGLRIIFA	13612	WWNLLQYWSQELKNS	12957					
LLQYWSQEL	13613	WDDLRNLCLFSYHRL	12958					
LRNLCLFSY	13614	SIRLVSGFLALAWDD	12959					
LVSGFLALA	13615	IRLVSGFLALAWDDL	12960					
VSGFLALAW	13616	KVTFDPIPIHYCTPA	12961					
FDPIPIHYC	13617	GLRIIFAVLSIVNRV	12962					
IIFAVLSIV	13618	EYRLINCNTSAITQA	12963					
LINCNTSAI	13619							

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LLNATAIAV	13620	AVSLLNATAIAVAEG	12964								
LRIIFAVLS	13621	LIGLRIIFAVLSIVN	12965								
VITQACPKV	13622	NTSVITQACPKVSFE	12966								
YWWNLLQYW	13623	VLKYWWNLLQYWSQE	12967								
FAILKCNDK	13624	PAGFAILKCNDKKFN	12968								
IFAVLSIVN	13625	LRIIFAVLSIVNRVR	12969								
INCNTSAIT	13626	YRLINCNTSAITQAC	12970								
LNATAIAVA	13627	VSLLNATAIAVAEGT	12971								
WNSSWSNKS	13628	NVPWNSSWSNKSLDE	12972								
WNASWSNKS	13629	NVPWNASWSNKSYED	12973								
ICTTTVPWN	13630	GKLICTTTVPWNASW	12974								
LLKLTVWGI	13631	QQHLLKLTVWGIKQL	12975								
LYKYKVVEI	13632	RSELYKYKVVEIKPL	12976								
MFLGFLGAA	13633	LGAMFLGFLGAAGST	12977								
MHSFNCGGE	13634	EIVMHSFNCGGEFFY	12978								
YWSQELKNS	13635	LLQYWSQELKNSAVS	12979								
IGAVFLGFL	13636	AVGIGAVFLGFLGAA	12980								
LIAARTVEL	13637	DFILIAARTVELLGH	12981								
LICTTTVPW	13638	SGKLICTTTVPWNAS	12982								
LLNGSLAEG	13639	TQLLLNGSLAEGEII	12983								
YWGQELKNS	13640	LVWYWGQELKNSAIS	12984								
IAARTVELL	13641	FILIAARTVELLGHS	12985								
LFLGFLGAA	13642	IGALFLGFLGAAGST	12986								
LKNSAVSLL	13643	SQELKNSAVSLLNAT	12987								
VGIGAVFLG	13644	KRAVGIGAVFLGFLG	12988								
VSLLNATAI	13645	NSAVSLLNATAIAVA	12989								
YATGDIIGD	13646	QTFYATGDIIGDIRQ	12990								
IAIAVAEGT	13647	LDIIAIAVAEGTDRI	12991								
IHYCTPAGF	13648	PIPIHYCTPAGFAIL	12992								
ILGLVIICS	13649	GTLILGLVIICSASN	12993								
IWNNMTWME	13650	VDEIWNNMTWMEWER	12994								
LGLVIICSA	13651	TLILGLVIICSASNN	12995								
LRDFILIAA	13652	YHRLRDFILIAARTV	12996								
LTPLCVTLD	13653	CVKLTPLCVTLDCHN	12997								
MLQLTVWGI	13654	QQHMLQLTVWGIKQL	12998								
VEINCTRPN	13655	NESVEINCTRPNNNT	12999								
VRQLLSGIV	13656	TVQVRQLLSGIVQQQ	13000								
LILGLVIIC	13657	WGTLILGLVIICSAS	13001								
VGGHQAAMQ	13658	LNTVGGHQAAMQMLK	13002								
LLVQNANPD	13659	TETLLVQNANPDCKT	13003								
VQNANPDCK	13660	TLLVQNANPDCKTIL	13004								
LGLNKIVRM	13661	WIILGLNKIVRMYSP	13005	0.0400	0.3300	0.1100	1.1000	0.0310	0.0290	0.3700	0.2400
LSEGATPQD	13662	FSALSEGATPQDLNT	13006								
WIILGLNKI	13663	YKRWIILGLNKIVRM	13007	1.2000	1.6000	0.7800	1.1000	0.0740	0.2400	0.3100	1.5000
LEEMMTACQ	13664	GATLEEMMTACQGVG	13008								
YKRWIILGL	13665	GEIYKRWIILGLNKI	13009	0.0610	0.0660	0.0890	-0.0043	0.0300	0.1000	0.0940	0.1800
IYKRWIILG	13666	VGEIYKRWIILGLNK	13010								
VSQNYPIVQ	13667	SSQVSQNYPIVQNLQ	13011								
WEKIRLRPG	13668	LDKWEKIRLRPGGKK	13012								
IAGTTSTLQ	13669	GSDIAGTTSTLQEQI	13013								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LLNATAIAV	13620	AVSLLNATAIAVAEG	12964					
LRIIFAVLS	13621	LIGLRIIFAVLSIVN	12965					
VITQACPKV	13622	NTSVITQACPKVSFE	12966					
YWWNLLQYW	13623	VLKYWWNLLQYWSQE	12967					
FAILKCNDK	13624	PAGFAILKCNDKKFN	12968					
IFAVLSIVN	13625	LRIIFAVLSIVNRVR	12969					
INCNTSAIT	13626	YRLINCNTSAITQAC	12970					
LNATAIAVA	13627	VSLLNATAIAVAEGT	12971					
WNSSWSNKS	13628	NVPWNSSWSNKSLDE	12972					
WNASWSNKS	13629	NVPWNASWSNKSYED	12973					
ICTTTVPWN	13630	GKLICTTTVPWNASW	12974					
LLKLTVWGI	13631	QQHLLKLTVWGIKQL	12975					
LYKYKVVEI	13632	RSELYKYKVVEIKPL	12976					
MFLGFLGAA	13633	LGAMFLGFLGAAGST	12977					
MHSFNCGGE	13634	EIVMHSFNCGGEFFY	12978					
YWSQELKNS	13635	LLQYWSQELKNSAVS	12979					
IGAVFLGFL	13636	AVGIGAVFLGFLGAA	12980					
LIAARTVEL	13637	DFILIAARTVELLGH	12981					
LICTTTVPW	13638	SGKLICTTTVPWNAS	12982					
LLNGSLAEG	13639	TQLLLNGSLAEGEII	12983					
YWGQELKNS	13640	LVWYWGQELKNSAIS	12984					
IAARTVELL	13641	FILIAARTVELLGHS	12985					
LFLGFLGAA	13642	IGALFLGFLGAAGST	12986					
LKNSAVSLL	13643	SQELKNSAVSLLNAT	12987					
VGIGAVFLG	13644	KRAVGIGAVFLGFLG	12988					
VSLLNATAI	13645	NSAVSLLNATAIAVA	12989					
YATGDIIGD	13646	QTFYATGDIIGDIRQ	12990					
IAIAVAEGT	13647	LDIIAIAVAEGTDRI	12991					
IHYCTPAGF	13648	PIPIHYCTPAGFAIL	12992					
ILGLVIICS	13649	GTLILGLVIICSASN	12993					
IWNNMTWME	13650	VDEIWNNMTWMEWER	12994					
LGLVIICSA	13651	TLILGLVIICSASNN	12995					
LRDFILIAA	13652	YHRLRDFILIAARTV	12996					
LTPLCVTLD	13653	CVKLTPLCVTLDCHN	12997					
MLQLTVWGI	13654	QQHMLQLTVWGIKQL	12998					
VEINCTRPN	13655	NESVEINCTRPNNNT	12999					
VRQLLSGIV	13656	TVQVRQLLSGIVQQQ	13000					
LILGLVIIC	13657	WGTLILGLVIICSAS	13001					
VGGHQAAMQ	13658	LNTVGGHQAAMQMLK	13002					
LLVQNANPD	13659	TETLLVQNANPDCKT	13003					
VQNANPDCK	13660	TLLVQNANPDCKTIL	13004					
LGLNKIVRM	13661	WIILGLNKIVRMYSP	13005	1.8000	0.0088	0.2800	0.0024	
LSEGATPQD	13662	FSALSEGATPQDLNT	13006					
WIILGLNKI	13663	YKRWIILGLNKIVRM	13007	4.0000	0.1200	0.5400	0.6200	
LEEMMTACQ	13664	GATLEEMMTACQGVG	13008					
YKRWIILGL	13665	GEIYKRWIILGLNKI	13009	0.0356	0.1300	0.7800	0.1400	
IYKRWIILG	13666	VGEIYKRWIILGLNK	13010					
VSQNYPIVQ	13667	SSQVSQNYPIVQNLQ	13011					
WEKIRLRPG	13668	LDKWEKIRLRPGGKK	13012					
IAGTTSTLQ	13669	GSDIAGTTSTLQEQI	13013					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
WASRELERF	13670	HLVWASRELERFALN	13014								
IPMFSALSE	13671	PEVIPMFSALSEGAT	13015								
MFSALSEGA	13672	VIPMFSALSEGATPQ	13016	0.0085		-0.0014		0.0058		-0.0010	
VIPMFSALS	13673	SPEVIPMFSALSEGA	13017	0.0460	0.0280	0.0034	-0.0043	0.1600		0.0075	-0.0045
MYSPVSILD	13674	IVRMYSPVSILDIRQ	13018								
IVRMYSPVS	13675	LNKIVRMYSPVSILD	13019								
VRMYSPVSI	13676	NKIVRMYSPVSILDI	13020								
YSPVSILDI	13677	VRMYSPVSILDIRQG	13021								
MTETLLVQN	13678	KNWMTETLLVQNANP	13022								
WMTETLLVQ	13679	VKNWMTETLLVQNAN	13023	0.0033	0.0130	0.0077	-0.0043	0.0480		-0.0010	-0.0045
ISPRTLNAW	13680	HQAISPRTLNAWVKV	13024								
VKNWMTETL	13681	TQEVKNWMTETLLVQ	13025								
IKCFNCGKE	13682	QKRIKCFNCGKEGHI	13026								
IPVGEIYKR	13683	NPPIPVGEIYKRWII	13027								
YTAVFMQRG	13684	KGGYTAVFMQRGQNP	13028								
VATLYCVHQ	13685	YNTVATLYCVHQRIE	13029								
WDRLHPVHA	13686	AAEWDRLHPVHAGPI	13030								
FLQSRPEPT	13687	PGNFLQSRPEPTAPP	13031	0.0970		0.0170		0.0190		0.0015	
FKTLRAEQA	13688	DRFFKTLRAEQATQE	13032								
MVHQAISPR	13689	QGQMVHQAISPRTLN	13033	0.0690	0.1400	1.5000	0.0170	0.8300	0.0950	-0.0010	0.0048
VHQAISPRT	13690	GQMVHQAISPRTLNA	13034	0.0003		0.0023		0.0034		-0.0010	
YKTLRAEQA	13691	DRFYKTLRAEQASQE	13035	0.0530	0.0016	0.0500		0.1500		0.0430	
VSILDIRQG	13692	YSPVSILDIRQGPKE	13036								
LAEAMSQVT	13693	ARVLAEAMSQVTNSA	13037								
LGKIWPSHK	13694	ANFLGKIWPSHKGRP	13038								
VKCFNCGKE	13695	RKTVKCFNCGKEGHI	13039								
YNTVATLYC	13696	RSLYNTVATLYCVHQ	13040								
LHPVHAGPI	13697	WDRLHPVHAGPIAPG	13041								
LYNTVATLY	13698	LRSLYNTVATLYCVH	13042								
MTDTLLVQN	13699	KNWMTDTLLVQNANP	13043								
WMTDTLLVQ	13700	VKNWMTDTLLVQNAN	13044								
IEVKDTKEA	13701	HQRIEVKDTKEALDK	13045								
LQGQMVHQA	13702	VQNLQGQMVHQAISP	13046								
MTNNPPIPV	13703	IGWMTNNPPIPVGEI	13047								
WMTNNPPIP	13704	QIGWMTNNPPIPVGE	13048								
IAPGQMREP	13705	AGPIAPGQMREPRGS	13049								
VHAGPIAPG	13706	LHPVHAGPIAPGQMR	13050								
LGPGATLEE	13707	LRALGPGATLEEMMT	13051								
VHAGPIPPG	13708	VHPVHAGPIPPGQMR	13052								
IPPGQMREP	13709	AGPIPPGQMREPRGS	13053								
LSPRTLNAW	13710	HQALSPRTLNAWVKV	13054								
YRLKHLVWA	13711	KKKYRLKHLVWASRE	13055								
LGPAATLEE	13712	LKALGPAATLEEMMT	13056								
LKALGPAAT	13713	KTILKALGPAATLEE	13057	0.0760		0.0100		-0.0023		-0.0010	
LKDKEPPLA	13714	QEQLKDKEPPLASLR	13058								
LSGGKLDAW	13715	ASVLSGGKLDAWEKI	13059								
MTSNPPIPV	13716	IGWMTSNPPIPVGEI	13060								
VKNWMTDTL	13717	TQDVKNWMTDTLLVQ	13061								
VSILDIKQG	13718	YSPVSILDIKQGPKE	13062								
WMTSNPPIP	13719	QIGWMTSNPPIPVGE	13063								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
WASRELERF	13670	HLVWASRELERFALN	13014					
IPMFSALSE	13671	PEVIPMFSALSEGAT	13015					
MFSALSEGA	13672	VIPMFSALSEGATPQ	13016		-0.0007			
VIPMFSALS	13673	SPEVIPMFSALSEGA	13017	0.0007	-0.0007	0.0130	0.0130	
MYSPVSILD	13674	IVRMYSPVSILDIRQ	13018					
IVRMYSPVS	13675	LNKIVRMYSPVSILD	13019					
VRMYSPVSI	13676	NKIVRMYSPVSILDI	13020					
YSPVSILDI	13677	VRMYSPVSILDIRQG	13021					
MTETLLVQN	13678	KNWMTETLLVQNANP	13022					
WMTETLLVQ	13679	VKNWMTETLLVQNAN	13023	0.0032	0.0280	0.0008	0.0053	
ISPRTLNAW	13680	HQAISPRTLNAWVKV	13024					
VKNWMTETL	13681	TQEVKNWMTETLLVQ	13025					
IKCFNCGKE	13682	QKRIKCFNCGKEGHL	13026					
IPVGEIYKR	13683	NPPIPVGEIYKRWII	13027					
YTAVFMQRG	13684	KGGYTAVFMQRGQNP	13028					
VATLYCVHQ	13685	YNTVATLYCVHQRIE	13029					
WDRLHPVHA	13686	AAEWDRLHPVHAGPI	13030					
FLQSRPEPT	13687	PGNFLQSRPEPTAPP	13031		0.0130			
FKTLRAEQA	13688	DRFFKTLRAEQATQE	13032					
MVHQAISPR	13689	QGQMVHQAISPRTLN	13033	0.0085	0.0550	0.0067	0.6400	
VHQAISPRT	13690	GQMVHQAISPRTLNA	13034		-0.0007			
YKTLRAEQA	13691	DRFYKTLRAEQASQE	13035	-0.0001	0.0028		-0.0015	
VSILDIRQG	13692	YSPVSILDIRQGPKE	13036					
LAEAMSQVT	13693	ARVLAEAMSQVTNSA	13037					
LGKIWPSHK	13694	ANFLGKIWPSHKGRP	13038					
VKCFNCGKE	13695	RKTVKCFNCGKEGHI	13039					
YNTVATLYC	13696	RSLYNTVATLYCVHQ	13040					
LHPVHAGPI	13697	WDRLHPVHAGPIAPG	13041					
LYNTVATLY	13698	LRSLYNTVATLYCVH	13042					
MTDTLLVQN	13699	KNWMTDTLLVQNANP	13043					
WMTDTLLVQ	13700	VKNWMTDTLLVQNAN	13044					
IEVKDTKEA	13701	HQRIEVKDTKEALDK	13045					
LQGQMVHQA	13702	VQNLQGQMVHQAISP	13046					
MTNNPPIPV	13703	IGWMTNNPPIPVGEI	13047					
WMTNNPPIP	13704	QIGWMTNNPPIPVGE	13048					
IAPGQMREP	13705	AGPIAPGQMREPRGS	13049					
VHAGPIAPG	13706	LHPVHAGPIAPGQMR	13050					
LGPGATLEE	13707	LRALGPGATLEEMMT	13051					
VHAGPIPPG	13708	VHPVHAGPIPPGQMR	13052					
IPPGQMREP	13709	AGPIPPGQMREPRGS	13053					
LSPRTLNAW	13710	HQALSPRTLNAWVKV	13054					
YRLKHLVWA	13711	KKKYRLKHLVWASRE	13055					
LGPAATLEE	13712	LKALGPAATLEEMMT	13056					
LKALGPAAT	13713	KTILKALGPAATLEE	13057		0.0006			
LKDKEPPLA	13714	QEQLKDKEPPLASLR	13058					
LSGGKLDAW	13715	ASVLSGGKLDAWEKI	13059					
MTSNPPIPV	13716	IGWMTSNPPIPVGEI	13060					
VKNWMTDTL	13717	TQDVKNWMTDTLLVQ	13061					
VSILDIKQG	13718	YSPVSILDIKQGPKE	13062					
WMTSNPPIP	13719	QIGWMTSNPPIPVGE	13063					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
FNTVATLYC	13720	KSLFNTVATLYCVHQ	13064								
IPMFTALSE	13721	PEVIPMFTALSEGAT	13065								
LASLKSLFG	13722	LYPLASLKSLFGNDP	13066								
LERFAVNPG	13723	SRELERFAVNPGLLE	13067								
LFNTVATLY	13724	LRSLFNTVATLYCVH	13068								
MFTALSEGA	13725	VIPMFTALSEGATPQ	13069								
WDRVHPVHA	13726	AAEWDRVHPVHAGPI	13070								
IVRMYSPTS	13727	LNKIVRMYSPTSILD	13071								
LERFALNPG	13728	SRELERFALNPGLLE	13072								
LQEQIAWMT	13729	TSTLQEQIAWMTGNP	13073								
VHPVHAGPI	13730	WDRVHPVHAGPIPPG	13074								
VIPMFTALS	13731	SPEVIPMFTALSEGA	13075								
VRMYSPTSI	13732	NKIVRMYSPTSILDI	13076								
LGKIWPSNK	13733	ANFLGKIWPSNKGRP	13077								
LTSLKSLFG	13734	LYPLTSLKSLFGNDP	13078								
MYSPTSILD	13735	IVRMYSPTSILDIRQ	13079								
YKLKHIVWA	13736	KKKYKLKHIVWASRE	13080								
YSPTSILDI	13737	VRMYSPTSILDIRQG	13081								
LTSLRSLFG	13738	LYPLTSLRSLFGNDP	13082								
MMLNIVGGH	13739	DLNMMLNIVGGHQAA	13083								
IDVKDTKEA	13740	HQRIDVKDTKEALDK	13084								
IGWMTSNPP	13741	QEQIGWMTSNPPIPV	13085								
IPVGDIYKR	13742	NPPIPVGDIYKRWII	13086								
LYPLASLKS	13743	DKELYPLASLKSLFG	13087								
VHQALSPRT	13744	GQMVHQALSPRTLNA	13088								
VNPGLLETS	13745	RFAVNPGLLETSEGC	13089								
YPLASLKSL	13746	KELYPLASLKSLFGN	13090								
FLQNRPEPT	13747	PGNFLQNRPEPTAPP	13091								
IMMQKSNFK	13748	AAAIMMQKSNFKGPR	13092								
LAEAMSQVQ	13749	ARVLAEAMSQVQQSN	13093								
LGKIWPSSK	13750	ANFLGKIWPSSKGRP	13094								
LNPGLLETA	13751	RFALNPGLLETAEGC	13095								
YPLASLRSL	13752	KELYPLASLRSLFGN	13096								
WQNYTPGPG	13753	FPDWQNYTPGPGIRY	13097								
VRPQVPLRP	13754	GFPVRPQVPLRPMTY	13098								
VPLRPMTYK	13755	RPQVPLRPMTYKGAF	13099								
LTFGWCFKL	13756	RYPLTFGWCFKLVPV	13100								
ILDLWVYHT	13757	RQEILDLWVYHTQGY	13101								
WCFKLVPVD	13758	TFGWCFKLVPVDPRE	13102								
LWVYHTQGY	13759	ILDLWVYHTQGYFPD	13103								
WSKSSIVGW	13760	GGKWSKSSIVGWPAI	13104								
ILDLWVYNT	13761	RQDILDLWVYNTQGY	13105								
LLHPMSQHG	13762	NNCLLHPMSQHGMDD	13106								
LLHPICQHG	13763	NNSLLHPICQHGMED	13107								
IRYPLTFGW	13764	GPGIRYPLTFGWCFK	13108								
ITSSNTAAT	13765	HGAITSSNTAATNAD	13109								
LEKHGAITS	13766	SRDLEKHGAITSSNT	13110								
LWVYHTQGF	13767	ILDLWVYHTQGFFPD	13111								
MTYKGAFDL	13768	LRPMTYKGAFDLSFF	13112								
LVPVDPREV	13769	CFKLVPVDPREVEEA	13113								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FNTVATLYC	13720	KSLFNTVATLYCVHQ	13064					
IPMFTALSE	13721	PEVIPMFTALSEGAT	13065					
LASLKSLFG	13722	LYPLASLKSLFGNDP	13066					
LERFAVNPG	13723	SRELERFAVNPGLLE	13067					
LFNTVATLY	13724	LRSLFNTVATLYCVH	13068					
MFTALSEGA	13725	VIPMFTALSEGATPQ	13069					
WDRVHPVHA	13726	AAEWDRVHPVHAGPI	13070					
IVRMYSPTS	13727	LNKIVRMYSPTSILD	13071					
LERFALNPG	13728	SRELERFALNPGLLE	13072					
LQEQIAWMT	13729	ISTLQEQIAWMTGNP	13073					
VHPVHAGPI	13730	WDRVHPVHAGPIPPG	13074					
VIPMFTALS	13731	SPEVIPMFTALSEGA	13075					
VRMYSPTSI	13732	NKIVRMYSPTSILDI	13076					
LGKIWPSNK	13733	ANFLGKIWPSNKGRP	13077					
LTSLKSLFG	13734	LYPLTSLKSLFGNDP	13078					
MYSPTSILD	13735	IVRMYSPTSILDIRQ	13079					
YKLKHIVWA	13736	KKKYKLKHIVWASRE	13080					
YSPTSILDI	13737	VRMYSPTSILDIRQG	13081					
LTSLRSLFG	13738	LYPLTSLRSLFGNDP	13082					
MMLNIVGGH	13739	DLNMMLNIVGGHQAA	13083					
IDVKDTKEA	13740	HQRIDVKDTKEALDK	13084					
IGWMTSNPP	13741	QEQIGWMTSNPPIPV	13085					
IPVGDIYKR	13742	NPPIPVGDIYKRWII	13086					
LYPLASLKS	13743	DKELYPLASLKSLFG	13087					
VHQALSPRT	13744	GQMVHQALSPRTLNA	13088					
VNPGLLETS	13745	RFAVNPGLLETSEGC	13089					
YPLASLKSL	13746	KELYPLASLKSLFGN	13090					
FLQNRPEPT	13747	PGNFLQNRPEPTAPP	13091					
IMMQKSNFK	13748	AAAIMMQKSNFKGPR	13092					
LAEAMSQVQ	13749	ARVLAEAMSQVQQSN	13093					
LGKIWPSSK	13750	ANFLGKIWPSSKGRP	13094					
LNPGLLETA	13751	RFALNPGLLETAEGC	13095					
YPLASLRSL	13752	KELYPLASLRSLFGN	13096					
WQNYTPGPG	13753	FPDWQNYTPGPGIRY	13097					
VRPQVPLRP	13754	GFPVRPQVPLRPMTY	13098					
VPLRPMTYK	13755	RPQVPLRPMTYKGAF	13099					
LTFGWCFKL	13756	RYPLTFGWCFKLVPV	13100					
ILDLWVYHT	13757	RQEILDLWVYHTQGY	13101					
WCFKLVPVD	13758	TFGWCFKLVPVDPRE	13102					
LWVYHTQGY	13759	ILDLWVYHTQGYFPD	13103					
WSKSSIVGW	13760	GGKWSKSSIVGWPAI	13104					
ILDLWVYNT	13761	RQDILDLWVYNTQGY	13105					
LLHPMSQHG	13762	NNCLLHPMSQHGMDD	13106					
LLHPICQHG	13763	NNSLLHPICQHGMED	13107					
IRYPLTFGW	13764	GPGIRYPLTFGWCFK	13108					
ITSSNTAAT	13765	HGAITSSNTAATNAD	13109					
LEKHGAITS	13766	SRDLEKHGAITSSNT	13110					
LWVYHTQGF	13767	ILDLWVYHTQGFFPD	13111					
MTYKGAFDL	13768	LRPMTYKGAFDLSFF	13112					
LVPVDPREV	13769	CFKLVPVDPREVEEA	13113					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VGWPAIRER	13770	SSIVGWPAIRERMRR	13114								
WCFKLVPVE	13771	TFGWCFKLVPVEPEK	13115								
FDSRLAFHH	13772	EWRFDSRLAFHHVAR	13116								
FKLVPVDPR	13773	GWCFKLVPVDPREVE	13117								
VPLRPMTFK	13774	RPQVPLRPMTFKGAF	13118								
LLDTGADDT	13775	KEALLDTGADDTVLE	13119	0.0001		-0.0015		-0.0023		-0.0010	
WMGYELHPD	13776	PFLWMGYELHPDKWT	13120								
YQYNVLPQG	13777	GIRYQYNVLPQGWKG	13121								
FRKYTAFTI	13778	DKDFRKYTAFTIPSI	13122								
WTVNDIQKL	13779	KDSWTVNDIQKLVGK	13123	0.0027		-0.0014		-0.0026		0.1200	
LDCTHLEGK	13780	IWQLDCTHLEGKHL	13124								
LDVGDAYFS	13781	VTVLDVGDAYFSVPL	13125	0.0003		-0.0014		-0.0026		-0.0007	
MDDLYVGSD	13782	YQYMDDLYVGSDLEI	13126	0.0006		-0.0014	-0.0160	0.0036		-0.0006	
VIPAETGQE	13783	EAEVIPAETGQETAY	13127								
WKGEGAVVI	13784	KLLWKGEGAVVIQDN	13128	0.4600	0.0011	0.0058	-0.0043	0.0750	0.0200	0.0060	-0.0045
WQLDCTHLE	13785	PGIWQLDCTHLEGKI	13129								
VDFRELNKR	13786	RKLVDFRELNKRTQD	13130								
WKPKMIGGI	13787	PGKWKPKMIGGIGGF	13131								
IWQLDCTHL	13788	SPGIWQLDCTHLEGK	13132	0.0013		-0.0021		0.0990		-0.0006	
VAVHIVASGY	13789	HLVAVHIVASGYIEA	13133								
WKGSPAIFQ	13790	PQGWKGSPAIFQSSM	13134	0.0010		-0.0014		-0.0026		-0.0007	
IGGYSAGER	13791	KGGIGGYSAGERIID	13135								
YALGHQAQ	13792	DSQYALGHQAQPDK	13136								
FWEVQLGIP	13793	TQDFWEVQLGIPHPA	13137								
IKKKDSTKW	13794	VFAIKKKDSTKWRKL	13138								
LGHQAQPD	13795	QYALGHQAQPDKSE	13139								
LGIPHPAGL	13796	EVQLGIPHPAGLKKK	13140	0.0020		0.1300		-0.0026		-0.0007	
VNTPPLVKL	13797	WEFVNTPPLVKLWYQ	13141	0.6900	0.0410	9.5000	0.0220	1.8000	1.9000	0.0630	0.2200
VTVLDVGDA	13798	KKSVTVLDVGDAYFS	13142	0.0019		-0.0014		0.0065		0.0030	
FPISPIETV	13799	TLNFPISPIETVPVK	13143	0.0190	0.0003	-0.0014	-0.0043	0.0350		-0.0007	0.0370
ISPIETVPV	13800	NFPISPIETVPVKLK	13144	0.0480	0.0013	0.0022	-0.0043	0.0810	0.0095	-0.0007	0.0460
FVNTPPLVK	13801	EWEFVNTPPLVKLWY	13145								
LNFPISPIE	13802	GCTLNFPISPIETVP	13146	0.0014		-0.0014		-0.0026		-0.0006	
WEFVNTPPL	13803	IPEWEFVNTPPLVKL	13147	1.1000	0.0089	1.8000	0.0920	0.6600	1.6000	0.0830	0.0540
IQNFRVYYR	13804	ITKIQNFRVYYRDSR	13148								
LVGPTPVNI	13805	GTVLVGPTPVNIIGR	13149	0.0066	0.0061	-0.0014	-0.0043	-0.0026		0.0043	-0.0045
VQLGIPHPA	13806	FWEVQLGIPHPAGLK	13150	0.0240		-0.0014		0.0033		-0.0006	
WQATWIPEW	13807	TEYWQATWIPEWEFV	13151								
IETVPVKLK	13808	ISPIETVPVKLKPGM	13152	0.0019		0.0140		-0.0026		-0.0007	
IGTVLVGPT	13809	KKAIGTVLVGPTPVN	13153								
LVAVHIVASG	13810	KHLVAVHIVASGYIE	13154								
VLVGPTPVN	13811	IGTVLVGPTPVNIIG	13155	0.0120	0.0170	-0.0003		0.0008	0.0030	-0.0004	
YIEAEVIPA	13812	ASGYIEAEVIPAETG	13156	0.0230	-0.0003	-0.0021	-0.0043	0.2300		0.0020	-0.0045
YVGSDLEIG	13813	DDLYVGSDLEIGQHR	13157								
MDGPKVKQW	13814	KPGMDGPKVKQWPLT	13158								
VASGYIEAE	13815	AVHVASGYIEAEVIP	13159								
VGPTPVNII	13816	TVLVGPTPVNIIGRN	13160	0.0010		-0.0014		-0.0026		0.0035	
VKQWPLTEE	13817	GPKVKQWPLTEEKIK	13161								
VYYRDSRDP	13818	NFRVYYRDSRDPIWK	13162								
WGFTTPDKK	13819	LLRWGFTTPDKKHQK	13163								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VGWPAIRER	13770	SSIVGWPAIRERMRR	13114					
WCFKLVPVE	13771	TFGWCFKLVPVEPEK	13115					
FDSRLAFHH	13772	EWRFDSRLAFHHVAR	13116					
FKLVPVDPR	13773	GWCFKLVPVDPREVE	13117					
VPLRPMTFK	13774	RPQVPLRPMTFKGAF	13118					
LLDTGADDT	13775	KEALLDTGADDTVLE	13119		-0.0003			
WMGYELHPD	13776	PFLWMGYELHPDKWT	13120					
YQYNVLPQG	13777	GIRYQYNVLPQGWKG	13121					
FRKYTAFTI	13778	DKDFRKYTAFTIPSI	13122					
WTVNDIQKL	13779	KDSWTVNDIQKLVGK	13123		-0.0005			
LDCTHLEGK	13780	IWQLDCTHLEGKHL	13124					
LDVGDAYFS	13781	VTVLDVGDAYFSVPL	13125		-0.0005			
MDDLYVGSD	13782	YQYMDDLYVGSDLEI	13126		-0.0005			
VIPAETGQE	13783	EAEVIPAETGQETAY	13127					
WKGEGAVVI	13784	KLLWKGEGAVVIQDN	13128	0.0450	0.2400	0.0450	0.2100	
WQLDCTHLE	13785	PGIWQLDCTHLEGKI	13129					
VDFRELNKR	13786	RKLVDFRELNKRTQD	13130					
WKPKMIGGI	13787	PGKWKPKMIGGIGGF	13131					
IWQLDCTHL	13788	SPGIWQLDCTHLEGK	13132		-0.0009			
VAVHVASGY	13789	HLVAVHVASGYIEA	13133					
WKGSPAIFQ	13790	PQGWKGSPAIFQSSM	13134		0.0087			
IGGYSAGER	13791	KGGIGGYSAGERIID	13135					
YALGIIQAQ	13792	DSQYALGIIQAQPDK	13136					
FWEVQLGIP	13793	TQDFWEVQLGIPHPA	13137					
IKKKDSTKW	13794	VFAIKKKDSTKWRKL	13138					
LGIIQAQPD	13795	QYALGIIQAQPDKSE	13139					
LGIPHPAGL	13796	EVQLGIPHPAGLKKK	13140		-0.0005			
VNTPPLVKL	13797	WEFVNTPPLVKLWYQ	13141	0.0390	1.7000	0.1400	1.9000	
VTVLDVGDA	13798	KKSVTVLDVGDAYFS	13142		-0.0005			
FPISPIETV	13799	TLNFPISPIETVPVK	13143	0.0150	0.0640	-0.0005	0.0016	
ISPIETVPV	13800	NFPISPIETVPVKLK	13144	0.0190	0.1500	0.0008	0.0046	
FVNTPPLVK	13801	EWEFVNTPPLVKLWY	13145					
LNFPISPIE	13802	GCTLNFPISPIETVP	13146		0.0380			
WEFVNTPPL	13803	IPEWEFVNTPPLVKL	13147	0.0230	1.4000	0.2600	2.6000	
IQNFRVYYR	13804	ITKIQNFRVYYRDSR	13148					
LVGPTPVNI	13805	GTVLVGPTPVNIIGR	13149	0.0290	0.0820	-0.0005	0.0180	
VQLGIPHPA	13806	FWEVQLGIPHPAGLK	13150		0.0024			
WQATWIPEW	13807	TEYWQATWIPEWEFV	13151					
IETVPVKLK	13808	ISPIETVPVKLKPGM	13152		0.0150			
IGTVLVGPT	13809	KKAIGTVLVGPTPVN	13153					
LVAVHVASG	13810	KHLVAVHVASGYIE	13154					
VLVGPTPVN	13811	IGTVLVGPTPVNIIG	13155	0.0400	0.0710	-0.0003	0.0320	
YIEAEVIPA	13812	ASGYIEAEVIPAETG	13156	0.0006	0.0120	0.0097	0.0480	
YVGSDLEIG	13813	DDLYVGSDLEIGQHR	13157					
MDGPKVKQW	13814	KPGMDGPKVKQWPLT	13158					
VASGYIEAE	13815	AVHVASGYIEAEVIP	13159					
VGPTPVNII	13816	FVLVGPTPVNIIGRN	13160		0.0150			
VKQWPLTEE	13817	GPKVKQWPLTEEKIK	13161					
VYYRDSRDP	13818	NFRVYYRDSRDPIWK	13162					
WGFTTPDKK	13819	LLRWGFTTPDKKHQK	13163					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VIYQYMDDL	13820	PEIVIYQYMDDLYVG	13164								
LKKKKSVTV	13821	PAGLKKKKSVTVLDV	13165	0.0060		-0.0014		-0.0026		-0.0006	
VPRRKAKII	13822	IKVVPRRKAKIIRDY	13166	0.0003		0.0700		-0.0024		2.5000	
FPQITLWQR	13823	SFSFPQITLWQRPLV	13167	0.0027				0.0130			
VIWGKTPKF	13824	ESIVIWGKTPKFRLP	13168								
YVDGAANRE	13825	ETFYVDGAANRETKL	13169								
FKNLKTGKY	13826	QEPFKNLKTGKYAKM	13170								
IQTKELQKQ	13827	ATDIQTKELQKQITK	13171								
YGKQMAGDD	13828	IRDYGKQMAGDDCVA	13172								
WRAMASDFN	13829	IISNWRAMASDFNLPP	13173	0.1500	0.0004	0.1600	-0.0030	4.7000	2.6000	0.2100	-0.0045
ISKIGPENP	13830	EGKISKIGPENPYNT	13174								
LTQIGCTLN	13831	RNLLTQIGCTLNFPI	13175								
IIQAQPDKS	13832	ALGIIQAQPDKSESE	13176	0.0001		-0.0014		-0.0026		-0.0007	
LPEKDSWTV	13833	PIVLPEKDSWTVNDI	13177								
FQSSMTKIL	13834	PAIFQSSMTKILEPF	13178	0.0320	0.0320	0.0200	-0.0043	0.0058	0.6500	0.0660	-0.0045
FTIPSINNE	13835	YTAFTIPSINNETPG	13179								
IFQSSMTKI	13836	SPAIFQSSMTKILEP	13180	0.0140	0.0420	0.0300	-0.0043	0.0140	0.3500	0.0270	0.0122
IIEQLIKKE	13837	VSQIIEQLIKKEKVY	13181								
LSWVPAIIKG	13838	KVYLSWVPAIIKGIGG	13182								
YLSWVPAIIK	13839	EKVYLSWVPAIIKGIG	13183								
YTAFTIPSI	13840	FRKYTAFTIPSINNE	13184	0.0270	0.1300	0.0048	-0.0043	0.1700	0.2800	0.0110	0.0089
IIATDIQTK	13841	IIDIIATDIQTKELQ	13185								
IWKGPAKLL	13842	RDPIWKGPAKLLWKG	13186								
LQKQITKIQ	13843	TKELQKQITKIQNFR	13187	0.0071	0.0210	0.0350		0.0540	0.0200	0.0530	
LKEALLDTG	13844	GGQLKEALLDTGADD	13188	0.0001		-0.0021		-0.0024		-0.0005	
VYLSWVPAH	13845	KEKVYLSWVPAIIKGI	13189								
FILKLAGRW	13846	TAYFILKLAGRWPVK	13190								
LEGKIILVA	13847	CTIILEGKIILVAVHV	13191								
YFILKLAGR	13848	ETAYFILKLAGRWPV	13192								
IILVAVHVA	13849	EGKIILVAVHVASGY	13193								
IWGKTPKFR	13850	SIVIWGKTPKFRLPI	13194								
LAGRWPVKV	13851	ILKLAGRWPVKVIHT	13195								
VVAKEIVAS	13852	LPPVVAKEIVASCDK	13196	0.0001		-0.0021		0.0043		-0.0010	
IDIIATDIQ	13853	ERIIDIIATDIQTKE	13197								
IIDIIATDI	13854	GERIIDIIATDIQTK	13198								
IIGRNMLTQ	13855	PVNIIGRNMLTQIGC	13199								
IKVKQLCKL	13856	YAGIKVKQLCKLLRG	13200								
VDKLVSSGI	13857	NEQVDKLVSSGIRKV	13201								
IVGAETFYV	13858	KEPIVGAETFYVDGA	13202								
LPPVVAKEI	13859	DFNLPPVVAKEIVAS	13203	0.0042		-0.0021		-0.0024		0.0036	
WTVQPIQLP	13860	PDKWTVQPIQLPEKD	13204								
FNLPPVVAK	13861	ASDFNLPPVVAKEIV	13205	0.0026		-0.0021		-0.0028		-0.0006	
FTSAAVKAA	13862	GSNFTSAAVKAACWW	13206								
LALQDSGLE	13863	AIIHLALQDSGLEVNI	13207								
LPPIVAKEI	13864	DFNLPPIVAKEIVAS	13208								
LQDSGLEVN	13865	HLALQDSGLEVNIVT	13209								
FNLPPIVAK	13866	ASDFNLPPIVAKEIV	13210								
IGQHRAKIE	13867	DLEIGQHRAKIEELR	13211								
IIGRNLLTQ	13868	PVNIIGRNLLTQIGC	13212	0.0059		-0.0014		0.0043		0.0990	
LEVNIVTDS	13869	DSGLEVNIVTDSQYA	13213	0.0001		-0.0014		0.0350		-0.0007	

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VIYQYMDDL	13820	PEIVIYQYMDDLYVG	13164					
LKKKKSVTV	13821	PAGLKKKKSVTVLDV	13165		0.0140			
VPRRKAKII	13822	IKVVPRRKAKIIRDY	13166		0.0030			
FPQITLWQR	13823	SFSFPQITLWQRPLV	13167		0.0006			
VIWGKTPKF	13824	ESIVIWGKTPKFRLP	13168					
YVDGAANRE	13825	ETFYVDGAANRETKL	13169					
FKNLKTGKY	13826	QEPFKNLKTGKYAKM	13170					
IQTKELQKQ	13827	ATDIQTKELQKQITK	13171					
YGKQMAGDD	13828	IRDYGKQMAGDDCVA	13172					
WRAMASDFN	13829	HSNWRAMASDFNLPP	13173	0.0008	0.0530	0.0250	0.0860	
ISKIGPENP	13830	EGKISKIGPENPYNT	13174					
LTQIGCTLN	13831	RNLLTQIGCTLNFPI	13175					
IIQAQPDKS	13832	ALGIIQAQPDKSESE	13176		-0.0005			
LPEKDSWTV	13833	PIVLPEKDSWTVNDI	13177					
FQSSMTKIL	13834	PAIFQSSMTKILEPF	13178	0.1100	0.7300	0.0140	0.9100	
FTIPSINNE	13835	YTAFTIPSINNETPG	13179					
IFQSSMTKI	13836	SPAIFQSSMTKILEP	13180	0.2800	0.3700	0.0150	2.3000	
IIEQLIKKE	13837	VSQIIEQLIKKEKVY	13181					
LSWVPAHKG	13838	KVYLSWVPAHKGIGG	13182					
YLSWVPAHK	13839	EKVYLSWVPAHKGIG	13183					
YTAFTIPSI	13840	FRKYTAFTIPSINNE	13184	-0.0004	0.8400	0.0610	1.9000	
IIATDIQTK	13841	IIDIIATDIQTKELQ	13185					
IWKGPAKLL	13842	RDPIWKGPAKLLWKG	13186					
LQKQITKIQ	13843	TKELQKQITKIQNFR	13187	0.0050	0.0055	0.0250	0.0028	
LKEALLDTG	13844	GGQLKEALLDTGADD	13188		-0.0009			
VYLSWVPAH	13845	KEKVYLSWVPAHKGI	13189					
FILKLAGRW	13846	TAYFILKLAGRWPVK	13190					
LEGKIILVA	13847	CTHLEGKIILVAVHV	13191					
YFILKLAGR	13848	ETAYFILKLAGRWPV	13192					
IILVAVHVA	13849	EGKIILVAVHVASGY	13193					
IWGKTPKFR	13850	SIVIWGKTPKFRLPI	13194					
LAGRWPVKV	13851	ILKLAGRWPVKVIHT	13195					
VVAKEIVAS	13852	LPPVVAKEIVASCDK	13196		-0.0009			
IDIIATDIQ	13853	ERIIDIIATDIQTKE	13197					
IIDIIATDI	13854	GERIIDIIATDIQTK	13198					
IIGRNMLTQ	13855	PVNIIGRNMLTQIGC	13199					
IKVKQLCKL	13856	YAGIKVKQLCKLLRG	13200					
VDKLVSSGI	13857	NEQVDKLVSSGIRKV	13201					
IVGAETFYV	13858	KEPIVGAETFYVDGA	13202					
LPPVVAKEI	13859	DFNLPPVVAKEIVAS	13203		0.0530			
WTVQPIQLP	13860	PDKWTVQPIQLPEKD	13204					
FNLPPVVAK	13861	ASDFNLPPVVAKEIV	13205		0.0840			
FTSAAVKAA	13862	GSNFTSAAVKAACWW	13206					
LALQDSGLE	13863	AIHLALQDSGLEVNI	13207					
LPPIVAKEI	13864	DFNLPPIVAKEIVAS	13208					
LQDSGLEVN	13865	HLALQDSGLEVNIVT	13209					
FNLPPIVAK	13866	ASDFNLPPIVAKEIV	13210					
IGQHRAKIE	13867	DLEIGQHRAKIEELR	13211					
IIGRNLLTQ	13868	PVNIIGRNLLTQIGC	13212		-0.0005			
LEVNIVTDS	13869	DSGLEVNIVTDSQYA	13213		-0.0005			

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LRGAKALTD	13870	CKLLRGAKALTDIVP	13214								
LVSSGIRKV	13871	VDKLVSSGIRKVLFL	13215								
FLLKLAGRW	13872	TAYFLLKLAGRWPVK	13216								
LALQDSGSE	13873	AIHLALQDSGSEVNI	13217								
LQDSGSEVN	13874	HLALQDSGSEVNIVT	13218								
VKVIHTDNG	13875	RWPVKVIHTDNGSNF	13219								
WPVKVIHTD	13876	AGRWPVKVIHTDNGS	13220								
YFLLKLAGR	13877	ETAYFLLKLAGRWPV	13221	0.0610				0.0210			
ICGKKAIGT	13878	LIEICGKKAIGTVLV	13222								
IVAKEIVAS	13879	LPPIVAKEIVASCDK	13223								
LRWGFTTPD	13880	QHLLRWGFTTPDKKH	13224								
LEGKVILVA	13881	CTHLEGKVILVAVHV	13225								
LKWGFTTPD	13882	EHLLKWGFTTPDKKH	13226								
VILVAVHVA	13883	EGKVILVAVHVASGY	13227								
LAWVPAHKG	13884	KVYLAWVPAHKGIGG	13228	0.6000	0.3700	0.8200	0.0049	0.3200	0.2300	0.2800	0.0240
YDQILIEIC	13885	VRQYDQILIEICGKK	13229								
YLAWVPAHK	13886	EKVYLAWVPAHKGIG	13230	1.4000	0.4400	4.1000	0.0930	5.4000	1.4000	0.5400	0.0460
IGQHRTKIE	13887	DLEIGQHRTKIEELR	13231								
IGRNLLTQI	13888	VNHGRNLLTQIGCT	13232	0.0027		-0.0014		0.0620		0.0067	
LWQRPLVTI	13889	QITLWQRPLVTIKIG	13233								
VSLTETTNQ	13890	QKVVSLTETTNQKTE	13234								
VYLAWVPAH	13891	KEKVYLAWVPAHKGI	13235								
ICGHKAIGT	13892	LIEICGHKAIGTVLV	13236								
LRGTKALTE	13893	CKLLRGTKALTEVIP	13237								
LVNQHEQL	13894	ESELVNQHEQLIKK	13238								
LVSQHEQL	13895	ESELVSQHEQLIKK	13239	0.0059		0.0210		0.0095		0.0009	
YFSVPLDKD	13896	GDAYFSVPLDKDFRK	13240								
IGRNMLTQI	13897	VNHGRNMLTQIGCT	13241								
IKVRQLCKL	13898	YPGIKVRQLCKLLRG	13242								
LWKGPAKLL	13899	RDPLWKGPAKLLWKG	13243								
LWQRPLVTV	13900	QITLWQRPLVTVKIG	13244								
YAGIKVKQL	13901	SQIYAGIKVKQLCKL	13245								
IWGKTPKFK	13902	SIVIWGKTPKFKLPI	13246								
LREHLLKWG	13903	IEELREHLLKWGFTT	13247								
VQPIQLPEK	13904	KWTVQPIQLPEKDSW	13248								
WQRPLVTIK	13905	ITLWQRPLVTIKIGG	13249								
HQAQPDRS	13906	ALGHQAQPDRSESE	13250								
LQAIHLALQ	13907	KTELQAIHLALQDSG	13251								
LVEICTEME	13908	IKALVEICTEMEKEG	13252								
LRQHLLRWG	13909	IEELRQHLLRWGFTT	13253								
LTQLGCTLN	13910	RNMLTQLGCTLNFPI	13254								
LVSAGIRKV	13911	VDKLVSAGIRKVLFL	13255	0.0039		0.1500		-0.0026		0.0045	
VDKLVSAGI	13912	NEQVDKLVSAGIRKV	13256	0.0024		0.5900		-0.0026		-0.0006	
YPGIKVRQL	13913	SQIYPGIKVRQLCKL	13257								
FRKQNPDIV	13914	LEPFRKQNPDIVIYQ	13258								
FSFPQITLW	13915	TVSFSFPQITLWQRP	13259								
FTSTTVKAA	13916	GSNFTSTTVKAACWW	13260								
HASDIQTK	13917	HDHASDIQTKELQ	13261								
LAGRWPVKT	13918	LLKLAGRWPVKTIHT	13262								
VQKIATESI	13919	TEAVQKIATESIVIW	13263								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LRGAKALTD	13870	CKLLRGAKALTDIVP	13214					
LVSSGIRKV	13871	VDKLVSSGIRKVLFL	13215					
FLLKLAGRW	13872	TAYFLLKLAGRWPVK	13216					
LALQDSGSE	13873	AIHLALQDSGSEVNI	13217					
LQDSGSEVN	13874	HLALQDSGSEVNIVT	13218					
VKVIHTDNG	13875	RWPVKVIHTDNGSNF	13219					
WPVKVIHTD	13876	AGRWPVKVIHTDNGS	13220					
YFLLKLAGR	13877	ETAYFLLKLAGRWPV	13221		0.0041			
ICGKKAIGT	13878	LIEICGKKAIGTVLV	13222					
IVAKEIVAS	13879	LPPIVAKEIVASCDK	13223					
LRWGFTTPD	13880	QHLLRWGFTTPDKKH	13224					
LEGKVILVA	13881	CTHLEGKVILVAVHV	13225					
LKWGFTTPD	13882	EHLLKWGFTTPDKKH	13226					
VILVAVHVA	13883	EGKVILVAVHVASGY	13227					
LAWVPAHKG	13884	KVYLAWVPAHKGIGG	13228	0.0014	0.1400	0.2500	0.3000	
YDQILIEIC	13885	VRQYDQILIEICGKK	13229					
YLAWVPAHK	13886	EKVYLAWVPAHKGIG	13230	0.0010	1.4000	1.6000	0.5200	
IGQHRTKIE	13887	DLEIGQHRTKIEELR	13231					
IGRNLLTQI	13888	VNHGRNLLTQIGCT	13232		0.0012			
LWQRPLVTI	13889	QITLWQRPLVTIKIG	13233					
VSLTETTNQ	13890	QKVVSLTETTNQKTE	13234					
VYLAWVPAH	13891	KEKVYLAWVPAHKGI	13235					
ICGHKAIGT	13892	LIEICGHKAIGTVLV	13236					
LRGTKALTE	13893	CKLLRGTKALTEVIP	13237					
LVNQHEQL	13894	ESELVNQHEQLIKK	13238					
LVSQHEQL	13895	ESELVSQHEQLIKK	13239		0.0040			
YFSVPLDKD	13896	GDAYFSVPLDKDFRK	13240					
IGRNMLTQI	13897	VNHGRNMLTQIGCT	13241					
IKVRQLCKL	13898	YPGIKVRQLCKLLRG	13242					
LWKGPAKLL	13899	RDPLWKGPAKLLWKG	13243					
LWQRPLVTV	13900	QITLWQRPLVTVKIG	13244					
YAGIKVKQL	13901	SQIYAGIKVKQLCKL	13245					
IWGKTPKFK	13902	SIVIWGKTPKFKLPI	13246					
LREHLLKWG	13903	IEELREHLLKWGFTT	13247					
VQPIQLPEK	13904	KWTVQPIQLPEKDSW	13248					
WQRPLVTIK	13905	ITLWQRPLVTIKIGG	13249					
IIQAQPDRS	13906	ALGIIQAQPDRSESE	13250					
LQAIHLALQ	13907	KTELQAIHLALQDSG	13251					
LVEICTEME	13908	IKALVEICTEMEKEG	13252					
LRQHLLRWG	13909	IEELRQHLLRWGFTT	13253					
LTQLGCTLN	13910	RNMLTQLGCTLNFPI	13254					
LVSAGIRKV	13911	VDKLVSAGIRKVLFL	13255		0.0120			
VDKLVSAGI	13912	NEQVDKLVSAGIRKV	13256		0.0028			
YPGIKVRQL	13913	SQIYPGIKVRQLCKL	13257					
FRKQNPDIV	13914	LEPFRKQNPDIVIYQ	13258					
FSFPQITLW	13915	FVSFSFPQITLWQRP	13259					
FTSTTVKAA	13916	GSNFTSTTVKAACWW	13260					
IIASDIQTK	13917	IIDIIASDIQTKELQ	13261					
LAGRWPVKT	13918	LLKLAGRWPVKTIHT	13262					
VQKIATESI	13919	TEAVQKIATESIVIW	13263					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
FTIPSTNNE	13920	YTAFTIPSTNNETPG	13264								
LEDINLPGK	13921	DTVLEDINLPGKWKP	13265								
LTDIVPLTE	13922	AKALTDIVPLTEEAE	13266								
LVTIKIGGQ	13923	QRPLVTIKIGGQLKE	13267								
MRGAHTNDV	13924	YARMRGAHTNDVKQL	13268								
VKTIHTDNG	13925	RWPVKTIHTDNGSNF	13269								
VQPIVLPEK	13926	KWTVQPIVLPEKDSW	13270								
WPVKTIHTD	13927	AGRWPVKTIHTDNGS	13271								
WQRPLVTVK	13928	ITLWQRPLVTVKIGG	13272								
WTVQPIVLP	13929	PDKWTVQPIVLPEKD	13273								
YTAFTIPST	13930	FRKYTAFTIPSTNNE	13274								
IDIIASDIQ	13931	ERIIDIIASDIQTKE	13275								
IIDIIASDI	13932	GERIIDIIASDIQTK	13276								
IVDIIATDI	13933	GERIVDIIATDIQTK	13277	0.0031				0.0320			
LEEINLPGK	13934	DTVLEEINLPGKWKP	13278								
LQAIYLALQ	13935	KTELQAIYLALQDSG	13279								
LQKQIIKIQ	13936	TKELQKQIIKIQNFR	13280								
VDIIATDIQ	13937	ERIVDIIATDIQTKE	13281								
YDQIPIEIC	13938	VRQYDQIPIEICGKK	13282								
FNFPQITLW	13939	VPTFNFPQITLWQRP	13283								
IGRNMLTQL	13940	VNIIGRNMLTQLGCT	13284								
ISRIGPENP	13941	EGKISRIGPENPYNT	13285								
LTEVIPLTE	13942	TKALTEVIPLTEEAE	13286								
MESIVIWGK	13943	KIAMESIVIWGKTPK	13287								
VPRRKVKII	13944	IKVVPRRKVKIIRDY	13288								
VSFSFPQIT	13945	QGTVSFSFPQITLWQ	13289								
WYQLETEPI	13946	VKLWYQLETEPIVGA	13290								
YPGIKVKQL	13947	SQIYPGIKVKQLCKL	13291								
FPQGEAREF	13948	NLAFPQGEAREFPPE	13292								
LIEALLDTG	13949	GGQLIEALLDTGADD	13293								
VSLTDTTNQ	13950	QKVVSLTDTTNQKTE	13294								
WETWWTDYW	13951	KETWETWWTDYWQAT	13295								
YAKMRTAHT	13952	TGKYAKMRTAHTNDV	13296								
YKNLKTGKY	13953	QEPYKNLKTGKYARM	13297								
LQLPPLERL	13954	PVPLQLPPLERLTLD	13298								
VPLQLPPLE	13955	AEPVPLQLPPLERLT	13299								
LYQSNPPPS	13956	IKFLYQSNPPPSPEG	13300								
VRIIKILYQ	13957	LKAVRIIKILYQSNP	13301								
YQSNPPPSP	13958	KFLYQSNPPPSPEGT	13302								
LQLPPIERL	13959	PVPLQLPPIERLRLD	13303								
VPLQLPPIE	13960	AEPVPLQLPPIERLR	13304								
WNHPGSQPK	13961	LEPWNHPGSQPKTAC	13305								
FLNKGLGIS	13962	QVCFLNKGLGISYGR	13306								
WKHPGSQPK	13963	LEPWKHPGSQPKTAC	13307								
YCKKCCFHC	13964	NNCYCKKCCFHCQVC	13308								
YCKKCCYHC	13965	TNCYCKKCCYHCQVC	13309								
WNHPGSQPT	13966	LEPWNHPGSQPTTAC	13310								
MIVWQVDRM	13967	WQVMIVWQVDRMRIR	13311								
WQVMIVWQV	13968	ENRWQVMIVWQVDRM	13312	3.3000		0.0059	0.0036	-0.0043	0.0690	1.9000	0.0032	-0.0045
WQVDRMRIR	13969	MIVWQVDRMRIRTWK	13313								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FTIPSTNNE	13920	YTAFTIPSTNNETPG	13264					
LEDINLPGK	13921	DTVLEDINLPGKWKP	13265					
LTDIVPLTE	13922	AKALTDIVPLTEEAE	13266					
LVTIKIGGQ	13923	QRPLVTIKIGGQLKE	13267					
MRGAHTNDV	13924	YARMRGAHTNDVKQL	13268					
VKTIHTDNG	13925	RWPVKTIHTDNGSNF	13269					
VQPIVLPEK	13926	KWTVQPIVLPEKDSW	13270					
WPVKTIHTD	13927	AGRWPVKTIHTDNGS	13271					
WQRPLVTVK	13928	TTLWQRPLVTVKIGG	13272					
WTVQPIVLP	13929	PDKWTVQPIVLPEKD	13273					
YTAFTIPST	13930	FRKYTAFTIPSTNNE	13274					
IDIIASDIQ	13931	ERIIDIIASDIQTKE	13275					
IIDIIASDI	13932	GERIIDIIASDIQTK	13276					
IVDIIATDI	13933	GERIVDIIATDIQTK	13277		0.0026			
LEEINLPGK	13934	DTVLEEINLPGKWKP	13278					
LQAIYLALQ	13935	KTELQAIYLALQDSG	13279					
LQKQIIKIQ	13936	TKELQKQIIKIQNFR	13280					
VDIIATDIQ	13937	ERIVDIIATDIQTKE	13281					
YDQIPIEIC	13938	VRQYDQIPIEICGKK	13282					
FNFPQITLW	13939	VPTFNFPQITLWQRP	13283					
IGRNMLTQL	13940	VNIIGRNMLTQLGCT	13284					
ISRIGPENP	13941	EGKISRIGPENPYNT	13285					
LTEVIPLTE	13942	TKALTEVIPLTEEAE	13286					
MESIVIWGK	13943	KIAMESIVIWGKTPK	13287					
VPRRKVKII	13944	IKVVPRRKVKIIRDY	13288					
VSFSFPQIT	13945	QGTVSFSFPQITLWQ	13289					
WYQLETEPI	13946	VKLWYQLETEPIVGA	13290					
YPGIKVKQL	13947	SQIYPGIKVKQLCKL	13291					
FPQGEAREF	13948	NLAFPQGEAREFPPE	13292					
LIEALLDTG	13949	GGQLIEALLDTGADD	13293					
VSLTDTTNQ	13950	QKVVSLTDTTNQKTE	13294					
WETWWTDYW	13951	KETWETWWTDYWQAT	13295					
YAKMRTAHT	13952	TGKYAKMRTAHTNDV	13296					
YKNLKTGKY	13953	QEPYKNLKTGKYARM	13297					
LQLPPLERL	13954	PVPLQLPPLERLTLD	13298					
VPLQLPPLE	13955	AEPVPLQLPPLERLT	13299					
LYQSNPPPS	13956	IKFLYQSNPPPSPEG	13300					
VRIIKILYQ	13957	LKAVRIIKILYQSNP	13301					
YQSNPPPSP	13958	KFLYQSNPPPSPEGT	13302					
LQLPPIERL	13959	PVPLQLPPIERLRLD	13303					
VPLQLPPIE	13960	AEPVPLQLPPIERLR	13304					
WNHPGSQPK	13961	LEPWNHPGSQPKTAC	13305					
FLNKGLGIS	13962	QVCFLNKGLGISYGR	13306					
WKHPGSQPK	13963	LEPWKHPGSQPKTAC	13307					
YCKKCCFHC	13964	NNCYCKKCCFHCQVC	13308					
YCKKCCYHC	13965	TNCYCKKCCYHCQVC	13309					
WNHPGSQPT	13966	LEPWNHPGSQPTTAC	13310					
MIVWQVDRM	13967	WQVMIVWQVDRMRIR	13311					
WQVMIVWQV	13968	ENRWQVMIVWQVDRM	13312	0.0018	0.1200	0.1500	0.2900	
WQVDRMRIR	13969	MIVWQVDRMRIRTWK	13313					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LQYLALTAL	13970	VGSLQYLALTALIKP	13314								
LGHGVSIEW	13971	DWHLGHGVSIEWRLR	13315								
VDRMRIRTW	13972	VWQVDRMRIRTWNSL	13316								
YFDCFSESA	13973	HLYYFDCFSESAIRN	13317								
YWGLHTGER	13974	ITTYWGLHTGERDWH	13318								
IRTWNSLVK	13975	RMRIRTWNSLVKHHM	13319								
LGQGVSIEW	13976	DWHLGQGVSIEWRKK	13320								
LVKHHMYVS	13977	WNSLVKHHMYVSKKA	13321								
IPLGEARLV	13978	EVHIPLGEARLVVRT	13322								
LVKHHMYIS	13979	WKSLVKHHMYISGKA	13323								
YLALTALIK	13980	SLQYLALTALIKPKK	13324								
IRTWKSLVK	13981	RMRIRTWKSLVKHHM	13325								
LADQLIHLY	13982	DPDLADQLIHLYYFD	13326								
LALTALIKP	13983	LQYLALTALIKPKKI	13327								
VDPGLADQL	13984	STQVDPGLADQLIHL	13328								
LYYFDCFSE	13985	LIHLYYFDCFSESAI	13329								
FSESAIRKA	13986	FDCFSESAIRKAILG	13330								
LADQLHHMH	13987	EPGLADQLHHMHYFD	13331								
WQVDRMKIR	13988	LIVWQVDRMKIRTWN	13332								
FSDSAIRKA	13989	FDCFSDSAIRKAILG	13333								
FSESAIRNA	13990	FDCFSESAIRNAILG	13334								
IVSPRCEYQ	13991	LGHIVSPRCEYQAGH	13335								
LQYLALAAL	13992	VGSLQYLALAALITP	13336								
VDRMKIRTW	13993	VWQVDRMKIRTWNSL	13337								
YWGLQTGER	13994	IKTYWGLQTGERDWH	13338								
IPLGDARLV	13995	EVHIPLGDARLVITT	13339								
LQYLALKAL	13996	VGSLQYLALKALVTP	13340								
WQVDRMRIN	13997	MIVWQVDRMRINTWK	13341								
IKPKKIKPP	13998	TALIKPKKIKPPLPS	13342								
VDRMRINTW	13999	VWQVDRMRINTWKSL	13343								
IGCQHSRIG	14000	HFRIGCQHSRIGITR	13344								
WTLELLEEL	14001	YNEWTLELLEELKSE	13345								
ILQQLLFIH	14002	IIRILQQLLFIHFRI	13346	0.0054				0.0200			
FIHFRIGCQ	14003	QLLFIHFRIGCQHSR	13347								
YNEWTLELL	14004	REPYNEWTLELLEEL	13348								
FPRPWLHGL	14005	VRHFPRPWLHGLGQH	13349								
WEGVEAIIR	14006	GDTWEGVEAIIRILQ	13350								
LEELKSEAV	14007	LELLEELKSEAVRHF	13351								
WAGVEAIIR	14008	GDTWAGVEAIIRILQ	13352								
YGDTWAGVE	14009	YETYGDTWAGVEAII	13353								
IGCRHSRIG	14010	HFRIGCRHSRIGITR	13354								
FIIFRIGCR	14011	QLLFIHFRIGCRHSR	13355								
FVHFRIGCQ	14012	QLLFVHFRIGCQHSR	13356								
YGDTWTGVE	14013	YETYGDTWTGVEAII	13357								
FPRIWLHSL	14014	VRHFPRIWLHSLGQH	13358								
WALELLEEL	14015	YNEWALELLEELKNE	13359								
LVTLLSSSK	14016	EEWLVTLLSSSKLDQ	13360								
VTLLSSSKL	14017	EWLVTLLSSSKLDQG	13361								
IIAIVVWTI	14018	VVAIIAIVVWTIVFI	13362								
VDYRIVIVA	14019	LAKVDYRIVIVAFIV	13363								

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LQYLALTAL	13970	VGSLQYLALTALIKP	13314					
LGHGVSIEW	13971	DWHLGHGVSIEWRLR	13315					
VDRMRIRTW	13972	VWQVDRMRIRTWNSL	13316					
YFDCFSESA	13973	HLYYFDCFSESAIRN	13317					
YWGLHTGER	13974	ITTYWGLHTGERDWH	13318					
IRTWNSLVK	13975	RMRIRTWNSLVKHHM	13319					
LGQGVSIEW	13976	DWHLGQGVSIEWRKK	13320					
LVKHHMYVS	13977	WNSLVKHHMYVSKKA	13321					
IPLGEARLV	13978	EVHIPLGEARLVVRT	13322					
LVKHHMYIS	13979	WKSLVKHHMYISGKA	13323					
YLALTALIK	13980	SLQYLALTALIKPKK	13324					
IRTWKSLVK	13981	RMRIRTWKSLVKHHM	13325					
LADQLHHLY	13982	DPDLADQLHHLYYFD	13326					
LALTALIKP	13983	LQYLALTALIKPKKI	13327					
VDPGLADQL	13984	STQVDPGLADQLHHL	13328					
LYYFDCFSE	13985	LHHLYYFDCFSESAI	13329					
FSESAIRKA	13986	FDCFSESAIRKAILG	13330					
LADQLHHMH	13987	EPGLADQLHHMHYFD	13331					
WQVDRMKIR	13988	LIVWQVDRMKIRTWN	13332					
FSDSAIRKA	13989	FDCFSDSAIRKAILG	13333					
FSESAIRNA	13990	FDCFSESAIRNAILG	13334					
IVSPRCEYQ	13991	LGHIVSPRCEYQAGH	13335					
LQYLALAAL	13992	VGSLQYLALAALITP	13336					
VDRMKIRTW	13993	VWQVDRMKIRTWNSL	13337					
YWGLQTGER	13994	IKTYWGLQTGERDWH	13338					
IPLGDARLV	13995	EVHIPLGDARLVITT	13339					
LQYLALKAL	13996	VGSLQYLALKALVTP	13340					
WQVDRMRIN	13997	MIVWQVDRMRINTWK	13341					
IKPKKIKPP	13998	TALIKPKKIKPPLPS	13342					
VDRMRINTW	13999	VWQVDRMRINTWKSL	13343					
IGCQHSRIG	14000	HFRIGCQHSRIGITR	13344					
WTLELLEEL	14001	YNEWTLELLEELKSE	13345					
ILQQLLFIH	14002	IRILQQLLFIHFRI	13346		0.0084			
FIHFRIGCQ	14003	QLLFIHFRIGCQHSR	13347					
YNEWTLELL	14004	REPYNEWTLELLEEL	13348					
FPRPWLHGL	14005	VRHFPRPWLHGLGQH	13349					
WEGVEAIIR	14006	GDTWEGVEAIIRILQ	13350					
LEELKSEAV	14007	LELLEELKSEAVRHF	13351					
WAGVEAIIR	14008	GDTWAGVEAIIRILQ	13352					
YGDTWAGVE	14009	YETYGDTWAGVEAII	13353					
IGCRHSRIG	14010	HFRIGCRHSRIGITR	13354					
FIHFRIGCR	14011	QLLFIHFRIGCRHSR	13355					
FVHFRIGCQ	14012	QLLFVHFRIGCQHSR	13356					
YGDTWTGVE	14013	YETYGDTWTGVEAII	13357					
FPRIWLHSL	14014	VRHFPRIWLHSLGQH	13358					
WALELLEEL	14015	YNEWALELLEELKNE	13359					
LVTLLSSSK	14016	EEWLVTLLSSSKLDQ	13360					
VTLLSSSKL	14017	EWLVTLLSSSKLDQG	13361					
IIAIVVWTI	14018	VVAIIAIVVWTIVFI	13362					
VDYRIVIVA	14019	LAKVDYRIVIVAFIV	13363					

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LRQRKIDRL	14020	RKILRQRKIDRLIDR	13364								
IVVWTIVFI	14021	IIAIVVWTIVFIEYR	13365								
VVWTIVFIE	14022	IAIVVWTIVFIEYRK	13366								
IEYRKILRQ	14023	IVFIEYRKILRQRKI	13367								
ILAIVALVV	14024	SLYILAIVALVVAII	13368								
WTIVFIEYR	14025	IVVWTIVFIEYRKIL	13369								
LAIVALVVA	14026	LQILAIVALVVAGII	13370								

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LRQRKIDRL	14020	RKILRQRKIDRLIDR	13364					
IVVWTIVFI	14021	IIAIVVWTIVFIEYR	13365					
VVWTIVFIE	14022	IAIVVWTIVFIEYRK	13366					
IEYRKILRQ	14023	IVFIEYRKILRQRKI	13367					
ILAIVALVV	14024	SLYILAIVALVVAII	13368					
WTIVFIEYR	14025	IVVWTIVFIEYRKIL	13369					
LAIVALVVA	14026	LQILAIVALVVAGII	13370					

Table XXa

HIV DR 3a Motif Peptides

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	VPTDPNPQE	14027	53	83	HACVPTDPNPQEVVL	13371	85	12	19
ENV	YLKDQQLLG	14028	31	48	VERYLKDQQLLGIWG	13372	669	18	28
ENV	MHEDIISLW	14029	29	45	VEQMHEDIISLWDQS	13373	114	17	27
ENV	VSFEPIPIH	14030	29	45	CPKVSFEPIPIHYCA	13374	250	18	28
ENV	LAVERYLKD	14031	26	41	ARVLAVERYLKDQQL	13375	664	15	23
ENV	VKIEPLGVA	14032	23	36	YKVVKIEPLGVAPTK	13376	564	15	23
ENV	VWKEATTTL	14033	22	34	GVPVWKEATTTLFCA	13377	52	22	34
ENV	LAWDDLRSL	14034	20	31	FLALAWDDLRSLCLF	13378	849	19	30
ENV	LIEESQNQQ	14035	20	31	IYTLIEESQNQQEKN	13379	737	07	11
ENV	LGWEGLKYL	14036	09	29	GLRLGWEGLKYLWNL	13380	892	07	23
ENV	LELDKWASL	14037	18	28	QELLELDKWASLWNW	13381	753	07	11
ENV	YLRDQQLLG	14038	18	28	VERYLRDQQLLGIWG	13382	669	11	17
ENV	MWQEVGKAM	14039	15	23	IINMWQEVGKAMYAP	13383	492	12	19
ENV	IEEEGGERD	14040	13	20	PEGIEEEGGERDRDR	13384	827	08	13
ENV	MNNENNGTN	14041	01	20	INEMNNENNGTNSTW	13385	212	01	2
ENV	IEEEGGEQD	14042	12	19	LGRIEEEGGEQDKNR	13386	827	02	3
ENV	LAEEEVVIR	14043	12	19	NGSLAEEEVVIRSEN	13387	309	04	6
ENV	LALDKWASL	14044	11	17	QDLLALDKWASLWNW	13388	753	05	8
ENV	LAVERYLRD	14045	11	17	ARVLAVERYLRDQQL	13389	664	10	16
ENV	IRSENLTNN	14046	10	16	EIIIRSENLTNNVKT	13390	317	03	5
ENV	MEWEREIDN	14047	10	16	MTWMEWEREIDNYTS	13391	721	03	5
GAG	INEEAAEWD	14048	55	86	KETINEEAAEWDRLH	13392	223	18	28
GAG	FSPEVIPMF	14049	54	84	EKAFSPEVIPMFSAL	13393	182	36	56
GAG	VLAEAMSQV	14050	33	52	KARVLAEAMSQVTNS	13394	383	09	14
GAG	MLKDTINEE	14051	32	50	AMQMLKDTINEEAAE	13395	218	30	47
GAG	VVEEKAFSP	14052	28	44	WVKVVEEKAFSPEVI	13396	176	28	44
GAG	LRAEQATQE	14053	27	42	FKTLRAEQATQEVKN	13397	325	09	14
GAG	MLKETINEE	14054	23	36	AMQMLKETINEEAAE	13398	218	22	34
GAG	VIEEKAFSP	14055	21	33	WVKVIEEKAFSPEVI	13399	176	20	31
GAG	VLAEAMSQA	14056	16	25	KARVLAEAMSQASGA	13400	383	03	5
GAG	IEEEQNKSK	14057	15	23	LDKIEEEQNKSKKKA	13401	103	09	14
GAG	LRAEQATQD	14058	14	22	FKTLRAEQATQDVKN	13402	325	10	16
GAG	LRAEQASQE	14059	12	19	YKTLRAEQASQEVKN	13403	325	12	19
NEF	YFPDWQNYT	14060	36	56	TQGYFPDWQNYTPGP	13404	195	33	52
NEF	FLKEKGGLE	14061	30	47	LSHFLKEKGGLEGLI	13405	114	15	23
NEF	FLKEKGGLD	14062	26	41	LSFFLKEKGGLDGLI	13406	114	14	22
NEF	FFPDWQNYT	14063	17	27	TQGFFPDWQNYTPGP	13407	195	17	27
NEF	VSRDLEKHG	14064	11	17	VGAVSRDLEKHGAIT	13408	46	11	17
POL	YMDDLYVGS	14065	62	97	IYQYMDDLYVGSDLE	13409	369	59	92
POL	IGPENPYNT	14066	60	94	ISKIGPENPYNTPVF	13410	236	28	44
POL	LHPDKWTVQ	14067	60	94	GYELHPDKWTVQPIQ	13411	420	29	45
POL	IVTDSQYAL	14068	59	92	EVNIVTDSQYALGII	13412	684	58	91
POL	IPAETGQET	14069	58	91	AEVIPAETGQETAYF	13413	838	55	86
POL	LTEEKIKAL	14070	56	88	QWPLTEEKIKALTEI	13414	210	26	41
POL	IEAEVIPAE	14071	55	86	SGYIEAEVIPAETGQ	13415	833	51	80
POL	LFLDGIDKA	14072	55	86	RKVLFLDGIDKAQEE	13416	749	32	50
POL	VAKEIVASC	14073	54	86	PPVVAKEIVASCDKC	13417	781	22	34
POL	LKGEAMHGQ	14074	53	83	KCQLKGEAMHGQVDC	13418	794	47	73
POL	VGSDLEIGQ	14075	53	83	DLYVGSDLEIGQHRA	13419	375	28	44
POL	IIRDYGKQM	14076	50	78	KAKIIRDYGKQMAGD	13420	1017	36	56

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
POL	MASDFNLPP	14077	47	73	WRAMASDFNLPPVVA	13421	771	24	38
POL	FYVDGAANR	14078	43	67	AETFYVDGAANRETK	13422	629	33	52
POL	IHTDNGSNF	14079	42	66	VKVIHTDNGSNFTSA	13423	862	17	27
POL	ILKEPVHGV	14080	41	64	NREILKEPVHGVYYD	13424	495	36	56
POL	IYQEPFKNL	14081	40	63	TYQIYQEPFKNLKTG	13425	530	39	61
POL	VYYDPSKDL	14082	39	61	VHGVYYDPSKDLIAE	13426	506	26	41
POL	YVTDRGRQK	14083	39	61	KAGYVTDRGRQKVVS	13427	646	19	30
POL	LTEEAELEL	14084	37	58	IVPLTEEAELELAEN	13428	481	12	19
POL	VIQDNSDIK	14085	37	58	GAVVIQDNSDIKVVP	13429	999	37	58
POL	IATDIQTKE	14086	35	55	IDIIATDIQTKELQK	13430	953	22	34
POL	INNETPGIR	14087	32	51	IPSINNETPGIRYQY	13431	321	31	48
POL	LIAEIQKQG	14088	30	47	SKDLIAEIQKQGQGQ	13432	514	09	14
POL	ICTEMEKEG	14089	28	44	LVEICTEMEKEGKIS	13433	221	14	22
POL	VGAETFYVD	14090	28	44	EPIVGAETFYVDGAA	13434	624	20	31
POL	IQKETWETW	14091	27	42	RLPIQKETWETWWTD	13435	582	09	14
POL	IKQEFGIPY	14092	26	41	WAGIKQEFGIPYNPQ	13436	884	21	33
POL	MAGDDCVAG	14093	25	39	GKQMAGDDCVAGRQD	13437	1025	23	36
POL	IKKEKVYLA	14094	20	31	EQLIKKEKVYLAWVP	13438	715	19	30
POL	MAGDDCVAS	14095	19	30	GKQMAGDDCVASRQD	13439	1025	19	30
POL	VPLDKDFRK	14096	18	28	YFSVPLDKDFRKYTA	13440	304	18	29
POL	IQQEFGIPY	14097	16	25	WAGIQQEFGIPYNPQ	13441	884	11	17
POL	LEKEPIVGA	14098	16	25	WYQLEKEPIVGAETF	13442	618	16	25
POL	YQLEKEPIV	14099	16	25	KLWYQLEKEPIVGAE	13443	616	16	25
POL	IQKETWEAW	14100	15	23	KLPIQKETWEAWWTE	13444	582	05	8
POL	FSSEQTRAN	14101	14	22	AREFSSEQTRANSPT	13445	14	10	16
POL	IASDIQTKE	14102	14	22	IDIIASDIQTKELQK	13446	953	09	14
POL	IATESIVIW	14103	14	22	VQKIATESIVIWGKT	13447	564	11	17
POL	ILIEICGKK	14104	14	22	YDQILIEICGKKAIG	13448	146	13	20
POL	VLEEINLPG	14105	14	22	DDTVLEEINLPGKWK	13449	116	11	17
POL	IKKEKVYLS	14106	13	20	EQLIKKEKVYLSWVP	13450	715	07	11
POL	VLEDINLPG	14107	13	20	DDTVLEDINLPGKWK	13451	116	13	20
POL	VLPEKDSWT	14108	13	20	QPIVLPEKDSWTVND	13452	431	13	20
POL	VIQDNSEIK	14109	12	19	GAVVIQDNSEIKVVP	13453	999	12	19
POL	IIKDYGKQM	14110	11	17	KAKIIKDYGKQMAGA	13454	1017	06	9
TAT	VERETETDP	14111	11	17	KEKVERETETDPAVQ	13455	95	01	2
VIF	LTEDRWNKP	14112	28	44	VKKLTEDRWNKPQKT	13456	175	09	14
VIF	YYFDCFSES	14113	20	31	IHLYYFDCFSESAIR	13457	112	14	22
VIF	LVEDRWNKP	14114	11	17	VQKLVEDRWNKPQKT	13458	175	04	6
VIF	IDPDLADQL	14115	10	16	STQIDPDLADQLIHL	13459	100	10	16
VPR	LKNEAVRHF	14116	18	28	LEELKNEAVRHFPRP	13460	23	10	16
VPR	LKSEAVRHF	14117	15	23	LEELKSEAVRHFPRI	13461	23	07	11
VPR	YIYETYGDT	14118	14	22	LGQYIYETYGDTWAG	13462	42	07	11
VPR	LKQEAVRHF	14119	11	17	LEELKQEAVRHFPRP	13463	23	06	9

Table XXb

HLV DR 3a Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VPTDPNPQE	14027	HACVPTDPNPQEVVL	13371								
YLKDQQLLG	14028	VERYLKDQQLLGIWG	13372								
MHEDHSLW	14029	VEQMHEDHSLWDQS	13373								
VSFEPIPHI	14030	CPKVSFEPIPHIYCA	13374								
LAVERYLKD	14031	ARVLAVERYLKDQQL	13375								
VKIEPLGVA	14032	YKVVKIEPLGVAPTK	13376								
VWKEATTTL	14033	GVPVWKEATTTLFCA	13377								
LAWDDLRSL	14034	FLALAWDDLRSLCLF	13378								
LIEESQNQQ	14035	IYTLIEESQNQQEKN	13379								
LGWEGLKYL	14036	GLRLGWEGLKYLWNL	13380								
LELDKWASL	14037	QELLELDKWASLWNW	13381								
YLRDQQLLG	14038	VERYLRDQQLLGIWG	13382								
MWQEVGKAM	14039	HNMWQEVGKAMYAP	13383								
IEEEGGERD	14040	PEGIEEEGGERDRDR	13384								
MNNENNGTN	14041	INEMNNENNGTNSTW	13385								
IEEEGGEQD	14042	LGRIEEEGGEQDKNR	13386								
LAEEEVVIR	14043	NGSLAEEEVVIRSEN	13387								
LALDKWASL	14044	QDLLALDKWASLWNW	13388								
LAVERYLRD	14045	ARVLAVERYLRDQQL	13389								
IRSENLTNN	14046	EIIIRSENLTNNVKT	13390								
MEWEREIDN	14047	MTWMEWEREIDNYTS	13391								
INEEAAEWD	14048	KETINEEAAEWDRLH	13392								
FSPEVIPMF	14049	EKAFSPEVIPMFSAL	13393	0.0086		0.0015	-0.0130	0.0340		-0.0010	
VLAEAMSQV	14050	KARVLAEAMSQVTNS	13394	0.0080				0.0120			
MLKDTINEE	14051	AMQMLKDTINEEAAE	13395								
VVEEKAFSP	14052	WVKVVEEKAFSPEVI	13396	0.0006				0.0016			
LRAEQATQE	14053	FKTLRAEQATQEVKN	13397								
MLKETINEE	14054	AMQMLKETINEEAAE	13398								
VIEEKAFSP	14055	WVKVIEEKAFSPEVI	13399								
VLAEAMSQA	14056	KARVLAEAMSQASGA	13400								
IEEEQNKSK	14057	LDKIEEEQNKSKKKA	13401								
LRAEQATQD	14058	FKTLRAEQATQDVKN	13402								
LRAEQASQE	14059	YKTLRAEQASQEVKN	13403								
YFPDWQNYT	14060	TQGYFPDWQNYTPGP	13404				-0.0017				
FLKEKGGLE	14061	LSHFLKEKGGLEGLI	13405								
FLKEKGGLD	14062	LSFFLKEKGGLDGLI	13406								
FFPDWQNYT	14063	TQGFFPDWQNYTPGP	13407								
VSRDLEKHG	14064	VGAVSRDLEKHGAIT	13408								
YMDDLYVGS	14065	IYQYMDDLYVGSDLE	13409								
IGPENPYNT	14066	ISKIGPENPYNTPVF	13410	0.0001		-0.0014	-0.0130	-0.0026		-0.0006	
LHPDKWTVQ	14067	GYELHPDKWTVQPIQ	13411								
IVTDSQYAL	14068	EVNIVTDSQYALGII	13412	0.0002	0.0034	-0.0010	0.4100	-0.0055		-0.0006	
IPAETGQET	14069	AEVIPAETGQETAYF	13413				-0.0033				
LTEEKIKAL	14070	QWPLTEEKIKALTEI	13414								
IEAEVIPAE	14071	SGYIEAEVIPAETGQ	13415								
LFLDGIDKA	14072	RKVLFLDGIDKAQEE	13416								
VAKEIVASC	14073	PPVVAKEIVASCDKC	13417	0.0001		-0.0021	-0.0130	0.0085		-0.0006	
LKGEAMHGQ	14074	KCQLKGEAMHGQVDC	13418				-0.0017				
VGSDLEIGQ	14075	DLYVGSDLEIGQHRA	13419								
IIRDYGKQM	14076	KAKIIRDYGKQMAGD	13420								

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VPTDPNPQE	14027	HACVPTDPNPQEVVL	13371					
YLKDQQLLG	14028	VERYLKDQQLLGIWG	13372					
MHEDHSLW	14029	VEQMHEDHSLWDQS	13373					
VSFEPIPIH	14030	CPKVSFEPIPIHYCA	13374					
LAVERYLKD	14031	ARVLAVERYLKDQQL	13375					
VKIEPLGVA	14032	YKVVKIEPLGVAPTK	13376					
VWKEATTTL	14033	GVPVWKEATTTLFCA	13377					
LAWDDLRSL	14034	FLALAWDDLRSLCLF	13378					
LIEESQNQQ	14035	IYTLIEESQNQQEKN	13379					
LGWEGLKYL	14036	GLRLGWEGLKYLWNL	13380					
LELDKWASL	14037	QELLELDKWASLWNW	13381					
YLRDQQLLG	14038	VERYLRDQQLLGIWG	13382					
MWQEVGKAM	14039	HNMWQEVGKAMYAP	13383					
IEEEGGERD	14040	PEGIEEEGGERDRDR	13384					
MNNENNGTN	14041	INEMNNENNGTNSTW	13385					
IEEEGGEQD	14042	LGRIEEEGGEQDKNR	13386					
LAEEEVVIR	14043	NGSLAEEEVVIRSEN	13387					
LALDKWASL	14044	QDLLALDKWASLWNW	13388					
LAVERYLRD	14045	ARVLAVERYLRDQQL	13389					
IRSENLTNN	14046	EHIRSENLTNNVKT	13390					
MEWEREIDN	14047	MTWMEWEREIDNYTS	13391					
INEEAAEWD	14048	KETINEEAAEWDRLH	13392					
FSPEVIPMF	14049	EKAFSPEVIPMFSAL	13393		0.0023			
VLAEAMSQV	14050	KARVLAEAMSQVTNS	13394		0.0025			
MLKDTINEE	14051	AMQMLKDTINEEAAE	13395					
VVEEKAFSP	14052	WVKVVEEKAFSPEVI	13396		0.0003			
LRAEQATQE	14053	FKTLRAEQATQEVKN	13397					
MLKETINEE	14054	AMQMLKETINEEAAE	13398					
VIEEKAFSP	14055	WVKVIEEKAFSPEVI	13399					
VLAEAMSQA	14056	KARVLAEAMSQASGA	13400					
IEEEQNKSK	14057	LDKIEEEQNKSKKKA	13401					
LRAEQATQD	14058	FKTLRAEQATQDVKN	13402					
LRAEQASQE	14059	YKTLRAEQASQEVKN	13403					
YFPDWQNYT	14060	TQGYFPDWQNYTPGP	13404					
FLKEKGGLE	14061	LSHFLKEKGGLEGLI	13405					
FLKEKGGLD	14062	LSFFLKEKGGLDGLI	13406					
FFPDWQNYT	14063	TQGFFPDWQNYTPGP	13407					
VSRDLEKHG	14064	VGAVSRDLEKHGAIT	13408					
YMDDLYVGS	14065	IYQYMDDLYVGSDLE	13409					
IGPENPYNT	14066	ISKIGPENPYNTPVF	13410		-0.0005			
LHPDKWTVQ	14067	GYELHPDKWTVQPIQ	13411					
IVTDSQYAL	14068	EVNIVTDSQYALGII	13412	0.0108	-0.0014	-0.0009		
IPAETGQET	14069	AEVIPAETGQETAYF	13413					
LTEEKIKAL	14070	QWPLTEEKIKALTEI	13414					
IEAEVIPAE	14071	SGYIEAEVIPAETGQ	13415					
LFLDGIDKA	14072	RKVLFLDGIDKAQEE	13416					
VAKEIVASC	14073	PPVVAKEIVASCDKC	13417		0.0015			
LKGEAMHGQ	14074	KCQLKGEAMHGQVDC	13418					
VGSDLEIGQ	14075	DLYVGSDLEIGQHRA	13419					
IIRDYGKQM	14076	KAKIIRDYGKQMAGD	13420					

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
MASDFNLPP	14077	WRAMASDFNLPPVVA	13421								
FYVDGAANR	14078	AETFYVDGAANRETK	13422	0.0021	-0.0005	0.0046	0.3900	0.0150		-0.0006	
IHTDNGSNF	14079	VKVIHTDNGSNFTSA	13423								
ILKEPVHGV	14080	NREILKEPVHGVYYD	13424	0.3000	0.1500	-0.0014	0.1000	0.1900	0.0300	-0.0007	0.0230
IYQEPFKNL	14081	TYQIYQEPFKNLKTG	13425				-0.0017				
VYYDPSKDL	14082	VHGVYYDPSKDLIAE	13426								
YVTDRGRQK	14083	KAGYVTDRGRQKVVS	13427								
LTEEAELEL	14084	IVPLTEEAELELAEN	13428								
VIQDNSDIK	14085	GAVVIQDNSDIKVVP	13429	0.0033	0.0280	0.0014	0.3000	-0.0055		-0.0006	
IATDIQTKE	14086	IDHATDIQTKELQK	13430								
INNETPGIR	14087	IPSINNETPGIRYQY	13431								
LIAEIQKQG	14088	SKDLIAEIQKQGQGQ	13432								
ICTEMEKEG	14089	LVEICTEMEKEGKIS	13433				-0.0017				
VGAETFYVD	14090	EPIVGAETFYVDGAA	13434								
IQKETWETW	14091	RLPIQKETWETWWTD	13435								
IKQEFGIPY	14092	WAGIKQEFGIPYNPQ	13436	0.0018	0.0018	0.1600	1.0000	0.0140		-0.0006	
MAGDDCVAG	14093	GKQMAGDDCVAGRQD	13437								
IKKEKVYLA	14094	EQLIKKEKVYLAWVP	13438	0.6400	0.0800	0.0059	0.0300	4.1000		0.0058	-0.0045
MAGDDCVAS	14095	GKQMAGDDCVASRQD	13439								
VPLDKDFRK	14096	YFSVPLDKDFRKYTA	13440								
IQQEFGIPY	14097	WAGIQQEFGIPYNPQ	13441								
LEKEPIVGA	14098	WYQLEKEPIVGAETF	13442								
YQLEKEPIV	14099	KLWYQLEKEPIVGAE	13443								
IQKETWEAW	14100	KLPIQKETWEAWWTE	13444								
FSSEQTRAN	14101	AREFSSEQTRANSPT	13445								
IASDIQTKE	14102	IDHASDIQTKELQK	13446								
IATESIVIW	14103	VQKIATESIVIWGKT	13447								
ILIEICGKK	14104	YDQILIEICGKKAIG	13448								
VLEEINLPG	14105	DDTVLEEINLPGKWK	13449								
IKKEKVYLS	14106	EQLIKKEKVYLSWVP	13450								
VLEDINLPG	14107	DDTVLEDINLPGKWK	13451								
VLPEKDSWT	14108	QPIVLPEKDSWTVND	13452								
VIQDNSEIK	14109	GAVVIQDNSEIKVVP	13453								
IIKDYGKQM	14110	KAKIIKDYGKQMAGA	13454								
VERETETDP	14111	KEKVERETETDPAVQ	13455								
LTEDRWNKP	14112	VKKLTEDRWNKPQKT	13456								
YYFDCFSES	14113	IHLYYFDCFSESAIR	13457								
LVEDRWNKP	14114	VQKLVEDRWNKPQKT	13458								
IDPDLADQL	14115	STQIDPDLADQLIHL	13459								
LKNEAVRHF	14116	LEELKNEAVRHFPRP	13460								
LKSEAVRHF	14117	LEELKSEAVRHFPRI	13461								
YIYETYGDT	14118	LGQYIYETYGDTWAG	13462								
LKQEAVRHF	14119	LEELKQEAVRHFPRP	13463								

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
MASDFNLPP	14077	WRAMASDFNLPPVVA	13421					
FYVDGAANR	14078	AETFYVDGAANRETK	13422	-0.0002	-0.0014	0.0035		
IITDNGSNF	14079	VKVIITDNGSNFTSA	13423					
ILKEPVHGV	14080	NREILKEPVHGVYYD	13424	0.0120	0.0033	0.0010	0.0210	
IYQEPFKNL	14081	TYQIYQEPFKNLKTG	13425					
VYYDPSKDL	14082	VHGVYYDPSKDLIAE	13426					
YVTDRGRQK	14083	KAGYVTDRGRQKVVS	13427					
LTEEAELEL	14084	IVPLTEEAELELAEN	13428					
VIQDNSDIK	14085	GAVVIQDNSDIKVVP	13429	0.0447	-0.0014	-0.0009		
IATDIQTKE	14086	IDIIATDIQTKELQK	13430					
INNETPGIR	14087	IPSINNETPGIRYQY	13431					
LIAEIQKQG	14088	SKDLIAEIQKQGQGQ	13432					
ICTEMEKEG	14089	LVEICTEMEKEGKIS	13433					
VGAETFYVD	14090	EPIVGAETFYVDGAA	13434					
IQKETWETW	14091	RLPIQKETWETWWTD	13435					
IKQEFGIPY	14092	WAGIKQEFGIPYNPQ	13436	0.0123	-0.0014	-0.0009		
MAGDDCVAG	14093	GKQMAGDDCVAGRQD	13437					
IKKEKVYLA	14094	EQLIKKEKVYLAWVP	13438	-0.0003	-0.0005	-0.0015	0.0011	
MAGDDCVAS	14095	GKQMAGDDCVASRQD	13439					
VPLDKDFRK	14096	YFSVPLDKDFRKYTA	13440					
IQQEFGIPY	14097	WAGIQQEFGIPYNPQ	13441					
LEKEPIVGA	14098	WYQLEKEPIVGAETF	13442					
YQLEKEPIV	14099	KLWYQLEKEPIVGAE	13443					
IQKETWEAW	14100	KLPIQKETWEAWWTE	13444					
FSSEQTRAN	14101	AREFSSEQTRANSPT	13445					
IASDIQTKE	14102	IDIIASDIQTKELQK	13446					
IATESIVIW	14103	VQKIATESIVIWGKT	13447					
ILIEICGKK	14104	YDQILIEICGKKAIG	13448					
VLEEINLPG	14105	DDTVLEEINLPGKWK	13449					
IKKEKVYLS	14106	EQLIKKEKVYLSWVP	13450					
VLEDINLPG	14107	DDTVLEDINLPGKWK	13451					
VLPEKDSWT	14108	QPIVLPEKDSWTVND	13452					
VIQDNSEIK	14109	GAVVIQDNSEIKVVP	13453					
IIKDYGKQM	14110	KAKIIKDYGKQMAGA	13454					
VERETETDP	14111	KEKVERETETDPAVQ	13455					
LTEDRWNKP	14112	VKKLTEDRWNKPQKT	13456					
YYFDCFSES	14113	IHLYYFDCFSESAIR	13457					
LVEDRWNKP	14114	VQKLVEDRWNKPQKT	13458					
IDPDLADQL	14115	STQIDPDLADQLIHL	13459					
LKNEAVRHF	14116	LEELKNEAVRHFPRP	13460					
LKSEAVRHF	14117	LEELKSEAVRHFPRI	13461					
YIYETYGDT	14118	LGQYIYETYGDTWAG	13462					
LKQEAVRHF	14119	LEELKQEAVRHFPRP	13463					

Table XXc
HIV DR 3b Motif Peptides

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ENV	MRDNWRSEL	14120	40	63	GGDMRDNWRSELYKY	13464	550	37	58
ENV	LTVQARQLL	14121	36	56	SITLTVQARQLLSGI	13465	620	27	42
ENV	IEAQQHLLQ	14122	35	55	LRAIEAQQHLLQLTV	13466	642	34	53
ENV	IIGDIRQAH	14123	27	44	TGEIIGDIRQAHCNI	13467	370	07	11
ENV	VEREKRAVG	14124	23	37	RRVVEREKRAVGIGA	13468	582	11	17
ENV	MVEQMHEDI	14125	23	36	KNNMVEQMHEDIISL	13469	110	19	30
ENV	AWDDLRSLC	14126	20	31	LALAWDDLRSLCLFS	13470	850	18	28
ENV	LEITTHSFN	14127	20	31	GGDLEITTHSFNCRG	13471	426	10	16
ENV	YDTEVHNVW	14128	18	28	AKAYDTEVHNVWATH	13472	71	15	23
ENV	AEGTDRIIE	14129	17	27	IAVAEGTDRIIEVVQ	13473	927	02	3
ENV	VQREKRAVG	14130	17	27	RRVVQREKRAVGIGA	13474	582	05	8
ENV	AEGTDRVIE	14131	15	23	IAVAEGTDRVIEVVQ	13475	927	07	11
ENV	IEAQQHLLK	14132	12	19	LRAIEAQQHLLKLTV	13476	642	08	13
ENV	LKCNDKKFN	14133	12	19	FAILKCNDKKFNGTG	13477	269	05	8
GAG	ANPDCKTIL	14134	45	70	VQNANPDCKTILKAL	13478	347	27	42
GAG	FYKTLRAEQ	14135	28	44	VDRFYKTLRAEQASQ	13479	321	19	30
GAG	APGQMREPR	14136	27	42	GPIAPGQMREPRGSD	13480	242	19	30
GAG	FFKTLRAEQ	14137	27	42	VDRFFKTLRAEQATQ	13481	321	26	41
GAG	IWPSHKGRP	14138	23	36	LGKIWPSHKGRPGNF	13482	470	22	34
GAG	LARNCRAPR	14139	20	32	EGHLARNCRAPRKKG	13483	431	19	30
GAG	IAKNCRAPR	14140	18	29	EGHIAKNCRAPRKKG	13484	431	10	16
GAG	ATQEVKNWM	14141	18	28	AEQATQEVKNWMTET	13485	330	14	22
GAG	ATQDVKNWM	14142	15	23	AEQATQDVKNWMTDT	13486	330	11	17
GAG	IARNCRAPR	14143	13	21	EGHIARNCRAPRKKG	13487	431	13	20
GAG	IWPSNKGRP	14144	13	20	LGKIWPSNKGRPGNF	13488	470	13	20
GAG	ANPDCKSIL	14145	11	17	VQNANPDCKSILRAL	13489	347	06	9
GAG	ASQEVKNWM	14146	11	17	AEQASQEVKNWMTET	13490	330	11	17
GAG	IWPSSKGRP	14147	10	16	LGKIWPSSKGRPGNF	13491	470	10	16
NEF	LIYSKKRQE	14148	18	28	LDGLIYSKKRQEILD	13492	171	11	17
NEF	VPVDPREVE	14149	11	17	FKLVPVDPREVEEAN	13493	227	06	9
NEF	MARELHPEY	14150	10	16	FHHMARELHPEYYKD	13494	316	04	6
POL	MGYELHPDK	14151	60	94	FLWMGYELHPDKWTV	13495	416	60	94
POL	FIHNFKRKG	14152	58	91	MAVFIHNFKRKGGIG	13496	930	57	89
POL	MNKELKKII	14153	56	89	VESMNKELKKIIGQV	13497	903	45	70
POL	IIGQVRDQA	14154	44	69	LKKIIGQVRDQAEHL	13498	910	43	67
POL	YHSNWRAMA	14155	39	61	HEKYHSNWRAMASDF	13499	764	23	36
POL	MEKEGKISK	14156	36	56	CTEMEKEGKISKIGP	13500	225	22	34
POL	YYRDSRDPI	14157	34	53	FRVYYRDSRDPIWKG	13501	975	34	54
POL	ANRETKLGK	14158	30	47	DGAANRETKLGKAGY	13502	635	28	44
POL	IGGQLKEAL	14159	25	39	TIKIGGQLKEALLDT	13503	99	17	27
POL	LDKDFRKYT	14160	19	30	SVPLDKDFRKYTAFT	13504	306	17	27
POL	YYRDSRDPL	14161	14	22	FRVYYRDSRDPLWKG	13505	975	13	21
POL	IIGQVREQA	14162	13	20	LKKIIGQVREQAEHL	13506	910	13	20
POL	YHNNWRAMA	14163	10	16	HEKYHNNWRAMASDF	13507	764	06	9
REV	ARRNRRRRW	14164	39	61	TRQARRNRRRRWRAR	13508	38	18	28
REV	ARKNRRRRW	14165	18	28	TRQARKNRRRRWRAR	13509	38	13	20
REV	LLKTVRLIK	14166	10	16	DEELLKTVRLIKFLY	13510	9	04	6
VIF	ISSEVHIPL	14167	27	42	HPRISSEVHIPLGDA	13511	48	08	13
VIF	VSSEVHIPL	14168	27	42	HPKVSSEVHIPLGEA	13512	48	11	17
VIF	VSIEWRLRR	14169	11	17	GHGVSIEWRLRRYST	13513	85	05	8

Table XXc
HIV DR 3b Motif Peptides

Protein	Core Sequence	Core SeqID Num	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
VPR	LPSNTRGRG	14170	01	50	IGILPSNTRGRGRRN	13514	82	01	2
VPR	LLEELKNEA	14171	17	27	TLELLEELKNEAVRH	13515	19	12	19
VPR	LLEELKSEA	14172	16	25	TLELLEELKSEAVRH	13516	19	15	23
VPU	AKVDYRIVI	14173	01	33	DLLAKVDYRIVIVAF	13517	3	01	2
VPU	AKVDYRLGV	14174	01	33	NFLAKVDYRLGVGAL	13518	3	01	2
VPU	ILRQRKIDR	14175	15	23	YRKILRQRKIDRLID	13519	42	12	19

Table XXd

HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num.	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
MRDNWRSEL	14120	GGDMRDNWRSELYKY	13464								
LTVQARQLL	14121	SITLTVQARQLLSGI	13465								
IEAQQHLLQ	14122	LRAIEAQQHLLQLTV	13466								
IIGDIRQAH	14123	TGEIIGDIRQAHCNI	13467								
VEREKRAVG	14124	RRVVEREKRAVGIGA	13468								
MVEQMHEDI	14125	KNNMVEQMHEDIISL	13469								
AWDDLRSLC	14126	LALAWDDLRSLCLFS	13470								
LEITTHSFN	14127	GGDLEITTHSFNCRG	13471								
YDTEVHNVW	14128	AKAYDTEVHNVWATH	13472								
AEGTDRIIE	14129	IAVAEGTDRIIEVVQ	13473								
VQREKRAVG	14130	RRVVQREKRAVGIGA	13474								
AEGTDRVIE	14131	IAVAEGTDRVIEVVQ	13475								
IEAQQHLLK	14132	LRAIEAQQHLLKLTV	13476								
LKCNDKKFN	14133	FAILKCNDKKFNGTG	13477								
ANPDCKTIL	14134	VQNANPDCKTILKAL	13478				0.0031				
FYKTLRAEQ	14135	VDRFYKTLRAEQASQ	13479				0.0049				
APGQMREPR	14136	GPIAPGQMREPRGSD	13480				-0.0017				
FFKTLRAEQ	14137	VDRFFKTLRAEQATQ	13481								
IWPSHKGRP	14138	LGKIWPSHKGRPGNF	13482								
LARNCRAPR	14139	EGHLARNCRAPRKKG	13483								
IAKNCRAPR	14140	EGHIAKNCRAPRKKG	13484								
ATQEVKNWM	14141	AEQATQEVKNWMTET	13485								
ATQDVKNWM	14142	AEQATQDVKNWMTDT	13486								
IARNCRAPR	14143	EGHIARNCRAPRKKG	13487								
IWPSNKGRP	14144	LGKIWPSNKGRPGNF	13488								
ANPDCKSIL	14145	VQNANPDCKSILRAL	13489								
ASQEVKNWM	14146	AEQASQEVKNWMTET	13490								
IWPSSKGRP	14147	LGKIWPSSKGRPGNF	13491								
LIYSKKRQE	14148	LDGLIYSKKRQEILD	13492								
VPVDPREVE	14149	FKLVPVDPREVEEAN	13493								
MARELHPEY	14150	FHHMARELHPEYYKD	13494								
MGYELHPDK	14151	FLWMGYELHPDKWTV	13495				-0.0017				
FIHNFKRKG	14152	MAVFIHNFKRKGGIG	13496	0.0009		1.3000	0.0470	0.0085		6.9000	
MNKELKKII	14153	VESMNKELKKIIGQV	13497								
IIGQVRDQA	14154	LKKIIGQVRDQAEHL	13498				0.0700				
YHSNWRAMA	14155	HEKYHSNWRAMASDF	13499				0.0022				
MEKEGKISK	14156	CTEMEKEGKISKIGP	13500				0.0110				
YYRDSRDPI	14157	FRVYYRDSRDPIWKG	13501								
ANRETKLGK	14158	DGAANRETKLGKAGY	13502				-0.0017				
IGGQLKEAL	14159	TIKIGGQLKEALLDT	13503				0.0090				
LDKDFRKYT	14160	SVPLDKDFRKYTAFT	13504								
YYRDSRDPL	14161	FRVYYRDSRDPLWKG	13505								
IIGQVREQA	14162	LKKIIGQVREQAEHL	13506								
YHNNWRAMA	14163	HEKYHNNWRAMASDF	13507								
ARRNRRRRW	14164	TRQARRNRRRRWRAR	13508								
ARKNRRRRW	14165	TRQARKNRRRRWRAR	13509								
LLKTVRLIK	14166	DEELLKTVRLIKFLY	13510								
ISSEVHIPL	14167	IIPRISSEVHIPLGDA	13511								
VSSEVHIPL	14168	HPKVSSEVHIPLGEA	13512								

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
MRDNWRSEL	14120	GGDMRDNWRSELYKY	13464					
LTVQARQLL	14121	SITLTVQARQLLSGI	13465					
IEAQQHLLQ	14122	LRAIEAQQHLLQLTV	13466					
IIGDIRQAH	14123	TGEIIGDIRQAHCNI	13467					
VEREKRAVG	14124	RRVVEREKRAVGIGA	13468					
MVEQMHEDI	14125	KNNMVEQMHEDHSL	13469					
AWDDLRSLC	14126	LALAWDDLRSLCLFS	13470					
LEITTHSFN	14127	GGDLEITTHSFNCRG	13471					
YDTEVHNVW	14128	AKAYDTEVHNVWATH	13472					
AEGTDRHE	14129	IAVAEGTDRHEVVQ	13473					
VQREKRAVG	14130	RRVVQREKRAVGIGA	13474					
AEGTDRVIE	14131	IAVAEGTDRVIEVVQ	13475					
IEAQQHLLK	14132	LRAIEAQQHLLKLTV	13476					
LKCNDKKFN	14133	FAILKCNDKKFNGTG	13477					
ANPDCKTIL	14134	VQNANPDCKTILKAL	13478					
FYKTLRAEQ	14135	VDRFYKTLRAEQASQ	13479					
APGQMREPR	14136	GPIAPGQMREPRGSD	13480					
FFKTLRAEQ	14137	VDRFFKTLRAEQATQ	13481					
IWPSHKGRP	14138	LGKIWPSHKGRPGNF	13482					
LARNCRAPR	14139	EGHLARNCRAPRKKG	13483					
IAKNCRAPR	14140	EGHIAKNCRAPRKKG	13484					
ATQEVKNWM	14141	AEQATQEVKNWMTET	13485					
ATQDVKNWM	14142	AEQATQDVKNWMTDT	13486					
IARNCRAPR	14143	EGHIARNCRAPRKKG	13487					
IWPSNKGRP	14144	LGKIWPSNKGRPGNF	13488					
ANPDCKSIL	14145	VQNANPDCKSILRAL	13489					
ASQEVKNWM	14146	AEQASQEVKNWMTET	13490					
IWPSSKGRP	14147	LGKIWPSSKGRPGNF	13491					
LIYSKKRQE	14148	LDGLIYSKKRQEILD	13492					
VPVDPREVE	14149	FKLVPVDPREVEEAN	13493					
MARELHPEY	14150	FHHMARELHPEYYKD	13494					
MGYELHPDK	14151	FLWMGYELHPDKWTV	13495					
FIHNFKRKG	14152	MAVFIHNFKRKGGIG	13496		0.0048			
MNKELKKII	14153	VESMNKELKKIIGQV	13497					
IIGQVRDQA	14154	LKKIIGQVRDQAEHL	13498					
YHSNWRAMA	14155	HEKYHSNWRAMASDF	13499					
MEKEGKISK	14156	CTEMEKEGKISKIGP	13500					
YYRDSRDPI	14157	FRVYYRDSRDPIWKG	13501					
ANRETKLGK	14158	DGAANRETKLGKAGY	13502					
IGGQLKEAL	14159	TIKIGGQLKEALLDT	13503					
LDKDFRKYT	14160	SVPLDKDFRKYTAFT	13504					
YYRDSRDPL	14161	FRVYYRDSRDPLWKG	13505					
IIGQVREQA	14162	LKKIIGQVREQAEHL	13506					
YHNNWRAMA	14163	HEKYHNNWRAMASDF	13507					
ARRNRRRRW	14164	TRQARRNRRRRWRAR	13508					
ARKNRRRRW	14165	TRQARKNRRRRWRAR	13509					
LLKTVRLIK	14166	DEELLKTVRLIKFLY	13510					
ISSEVHIPL	14167	HPRISSEVHIPLGDA	13511					
VSSEVHIPL	14168	HPKVSSEVHIPLGEA	13512					
VSIEWRLRR	14169	GHGVSIEWRLRRYST	13513					

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num.	DR1	DR2wß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VSIEWRLRR	14169	GHGVSIEWRLRRYST	13513								
LPSNTRGRG	14170	IGILPSNTRGRGRRN	13514								
LLEELKNEA	14171	TLELLEELKNEAVRH	13515								
LLEELKSEA	14172	TLELLEELKSEAVRH	13516								
AKVDYRIVI	14173	DLLAKVDYRIVIVAF	13517								
AKVDYRLGV	14174	NFLAKVDYRLGVGAL	13518								
ILRQRKIDR	14175	YRKILRQRKIDRLID	13519	0.0024	0.0740	0.0410	13.0000	-0.0055		0.1500	

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LPSNTRGRG	14170	IGILPSNTRGRGRRN	13514					
LLEELKNEA	14171	TLELLEELKNEAVRH	13515					
LLEELKSEA	14172	TLELLEELKSEAVRH	13516					
AKVDYRIVI	14173	DLLAKVDYRIVIVAF	13517					
AKVDYRLGV	14174	NFLAKVDYRLGVGAL	13518					
ILRQRKIDR	14175	YRKILRQRKIDRLID	13519	0.0016	-0.0014	0.0270		

--TABLE III

		POSITION									
MOTIFS		1° anchor 1	2	3	4	5	1° anchor 6	7	8	9	
DR4	preferred	FMY*LIVW*	M	T		I	VST*CPALIM*	MH		MH	
	deleterious				W			R		WDE	
DR1	preferred	MF*LIVWY*			PAMQ		VMAT*SPLIC*	M		AVM	
	deleterious		C	CH	FD	CWD		GDE	D		
DR7	preferred	MF*LIVWY*	M	W	A		IVMSA*CTPL*	M		IV	(SEQ ID NO:14527)
	deleterious		C		G			GRD	N	G	(SEQ ID NO:14528)
DR Supermotif		MF*LIVWY*					VMSTA*CPLI*				

DR3 MOTIFS	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6
motif a preferred	LIVMFY			D		
motif b preferred	LIVMFAY			DNQEST		KRH

Italicized residues indicate less preferred or "tolerated" residues.--

Table XXIII: Immunogenicity of HIV peptides

	Peptide	Seq ID	Sequence	Protein	Immunogenicity	
					patients	transgenic
A2 Supermotif	1261.04	14176	LTFGWCFKL	HIV nef 221	4/12	3/3
	1261.15	14177	MASDFNLPPV	hiv pol 774	1/15	2/6
	1069.32	14178	VLAEAMSQV	hiv gag 386	6/19	3/3
	1261.16	14179	CTLNFPISPI	hiv pol 182	0/1	1/6
	1261.02	14180	LLQLTVWGI	HIV env 651	2/8	1/6
	1261.13	14181	KLVGKLNWA	HIV pol 448	3/15	3/3
	1211.04	14182	KLTPLCVTL	HIV env 134	2/12	2/6
	1261.08	14183	ALVEICTEM	HIV pol 220	0/2	1/6
	1261.11	14184	AIIRILQQL	HIV vpr 59	5/9	0/6
	1261.09	14185	LVGPTPVNI	HIV pol 163	1/9	1/6
	1261.12	14186	RILQQLLFI	HIV vpr 62	6/20	2/6
	1261.05	14187	TLNFPISPI	HIV pol 183	1/7	0/6
	1261.03	14188	MTNNPPIPV	HIV gag 271	2/17	4/6
	1261.17	14189	KMIGGIGGFI	HIV pol 132	2/7	0/6
	941.03	14190	ILKEPVHGV	HIV pol 498	8/19	3/6
	1261.10	14191	RAMASDFNL	HIV pol 772	2/9	0/6
	1261.07	14192	KAACWWAGI	HIV pol 879	1/8	0/6
A3 Supermotif	1211.32	14193	KIQNFRVYYR	HIV pol 971	4/6	
	1193.03	14194	AVFIHNFKR	HIV pol 931	3/6	
	1069.49	14195	QMAVFIHNFK	HIV pol 929	3/6	
	1150.14	14196	MAVFIHNFK	HIV pol 930	6/6	
	1069.42	14197	KVYLAWVPAHK	HIV pol 722	6/6	
	966.01	14198	AIFQSSMTK	HIV pol 347	5/6	1/6
	940.03	14199	QVPLRPMTYK	HIV nef 100	0/6	6/10
	1273.07	14200	TTLFCASDAK	HIV env 61	3/6	
	1273.09	14201	VTIKIGGQLK	HIV pol 98	6/6	
	1069.43	14202	TVYYGVPVWK	HIV env 48		28/33
	1069.47	14203	VTVYYGVPVWK	HIV env 47	6/6	
DR Supermotif	27	14204	KRWILGLNKIVRMY	HIV gag 298	3/13	
	27	14205	GEIYKRWILGLNKI	HIV gag 294	2/13	
	27	14206	WEFVNTPPLVKLWYQ	HIV pol 596	2/13	
	27	14207	QKQITKIQNFRVYYR	HIV pol 956	3/13	
	1280	14208	KVYLAWVPAHKGIGG	HIV pol 712	3/13	
	27	14209	EKVYLAWVPAHKGIG	HIV pol 711	1/13	
	27	14210	QGQMVHQAISPRTLN	HIV gag 171	4/13	
	27	14211	SPAIFQSSMTKILEP	HIV pol 335	3/13	
	27	14212	FRKYTAFTIPSINNE	HIV pol 303	3/13	
	27	14213	HSNWRAMASDFNLPP	HIV pol 758	3/13	
	27	14214	KTAVQMAVFIHNFKR	HIV pol 915	4/13	

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		
				Source	Seq ID	Sequence
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	14215	YTAVVPLVY
	A2	A*0201	JY	HBVc 18-27 F6->Y	14216	FLPSDYFPSV
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	14217	FLPSDYFPSV
	A2	A*0203	FUN	HBVc 18-27 F6->Y	14218	FLPSDYFPSV
	A2	A*0206	CLA	HBVc 18-27 F6->Y	14219	FLPSDYFPSV
	A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	14220	FLPSDYFPSV
	A3		GM3107	non-natural (A3CON1)	14221	KVFPYALINK
	A11		BVR	non-natural (A3CON1)	14222	KVFPYALINK
	A24	A*2402	KAS116	non-natural (A24CON1)	14223	AYIDNYNKF
	A31	A*3101	SPACH	non-natural (A3CON1)	14224	KVFPYALINK
	A33	A*3301	LWAGS	non-natural (A3CON1)	14225	KVFPYALINK
	A28/68	A*6801	C1R	HBVc 141-151 T7->Y	14226	STLPETYVVRR
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	14227	FTQAGYPAL
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	14228	APRTLVYLL
	B8	B*0801	Steinlin	HIVgp 586-593 Y1->F, Q5->Y	14229	FLKDYQLL
	B27	B*2705	LG2	R 60s	14230	FRYNGLIHR
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	14231	FPFKYAAAF
	B35	B*3502	TISI	non-natural (B35CON2)	14232	FPFKYAAAF
	B35	B*3503	EHM	non-natural (B35CON2)	14233	FPFKYAAAF
	B44	B*4403	PITOUT	EF-1 G6->Y	14234	AEMGKYSFY
	B51		KAS116	non-natural (B35CON2)	14235	FPFKYAAAF
	B53	B*5301	AMAI	non-natural (B35CON2)	14236	FPFKYAAAF
	B54	B*5401	KT3	non-natural (B35CON2)	14237	FPFKYAAAF
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	14238	QYDDAVYKL
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	14239	YRHDGGNVL
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	14240	YRHDGGNVL
Mouse	D^b		EL4	Adenovirus E1A P7->Y	14241	SGPSNTYPEI
	K^b		EL4	VSV NP 52-59	14242	RGYVFQGL
	D^d		P815	HIV-IIIB ENV G4->Y	14243	RGPYRAFVTI
	K^d		P815	non-natural (KdCON1)	14244	KFNPMKTYI
	L^d		P815	HBVs 28-39	14245	IPQSLDSYWTSL

B. Class II binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		
				Source		Sequence
Human	DR1	DRB1*0101	LG2	HA Y307-319	14246	YPKYVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	14247	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	14248	YAAFAAAKTAAAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	14249	YKTIAFDEEARR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	14250	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	14251	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	14252	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	14253	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	14254	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	14255	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	14256	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	14257	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	14258	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	14259	EALIHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	14260	QYIKANAKFIGITE
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	14261	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	14262	PKYVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	14263	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	14264	YARFQSQTTLKQKT
	DQ3.1	DQA1*0301/DQB1*0301	PF	non-natural (ROIV)	14265	YAHAAHAAHAAHAAHAA
Mouse	IA^b		DB27.4	non-natural (ROIV)	14266	YAHAAHAAHAAHAAHAA
	IA^d		A20	non-natural (ROIV)	14267	YAHAAHAAHAAHAAHAA
	IA^k		CH-12	HEL 46-61	14268	YNTDGSTDYGILQINSR
	IA^s		LS102.9	non-natural (ROIV)	14269	YAHAAHAAHAAHAAHAA
	IA^u		91.7	non-natural (ROIV)	14270	YAHAAHAAHAAHAAHAA
	IE^d		A20	Lambda repressor 12-26	14271	YLEDARRKKAIYEKKK
	IE^k		CH-12	Lambda repressor 12-26	14272	YLEDARRKKAIYEKKK

TABLE XXVII

in vitro binding of conserved HIV derived peptides to HLA-A2 supertype alleles

peptide	AA	Protein	1st Position	Seq ID	sequence	Conservation (%) total	Conservation (%) B	A2-supertype binding capacity (IC50 nM) A*0201	A*0202	A*0203	A*0206	A*6802	alleles bound
1261.14	10	NEF	221	14273	LTFGWCFKLV	55	74	294.1	48.9	185.2	57.8	6.2	5
1261.04	9	NEF	221	14274	LTFGWCFKL	61	74	35.7	33.1	4545.5	205.6	5.6	4
1261.06	9	POL	316	14275	YTAFTIPSI	58	68	26.3	6.1	9.1	7	16.7	5
1261.15	10	POL	774	14276	MASDFNLPPV	39	68	62.5	22.6	55.6	33.6	18.2	5
1069.32	9	GAG	386	14277	VLAEAMSQV	52	74	66.6	82.7	15.2	115.6	363.6	5
1261.16	10	POL	182	14278	CTLNFPISPI	94	100	147	23.9	30.3	8.4	100	5
1261.02	9	ENV	651	14279	LLQLTVWGI	53	63	9.8	215	43.5	24.7	645.2	4
1261.13	9	POL	448	14280	KLVGKLNWA	95	95	59.5	12.6	5.9	39.8	3076.9	4
1211.04	9	ENV	134	14281	KLTPLCVTL	81	95	102	126.5	66.7	185	20000	4
1261.08	9	POL	220	14282	ALVEICTEM	23	79	217.3	187	140.8	264.3	2857.1	4
1261.11	9	VPR	59	14283	AIIRILQQL	61	74	333.3	22.6	41.7	38.5	547.9	4
1261.09	9	POL	163	14284	LVGPTPVNI	84	100	454.5	153.6	19.2	2846.2	67.8	4
1261.12	9	VPR	62	14285	RILQQLLFI	56	74	19.2	1535.7	125	37	1818.2	3
1261.05	9	POL	183	14286	TLNFPISPI	97	100	75.7	1482.8	1.1	1947.4	57.1	3
1261.03	9	GAG	271	14287	MTNNPPIPV	31	89	166.6	7166.7	33.3	1608.7	12.1	3
1261.17	10	POL	132	14288	KMIGGIGGFI	97	95	172.4	54.4	4.8	770.8	3333.3	3
941.03	9	POL	498	14289	ILKEPVHGV	64	79	192.3	2388.9	6.7	37000	363.6	3
1260.10	9	POL	772	14290	RAMASDFNL	64	79	217.3	116.2	25000	52.1	3076.9	3
1261.07	9	POL	879	14291	KAACWWAGI	49	79	277.7	1075	83.3	160.9	2666.7	3
1211.09	10	ENV	814	14292	SLLNATDIAV	22	68	9.8	1303	238.1	28.5	5479.4	3
1211.05	9	ENV	608	14293	FLGAAGSTM	86	100	73.5	3583.3	1.5	4111.1	66666.7	2
25.0053	9	VPR	66	14294	QLLFIHFRI	69	89	94.3	21500	25000	1608.7	476.2	2
25.0139	10	GAG	270	14295	WMTNNPPIPV	31	89	98	3071.4	16.9	18500	2222.2	2
1069.33	10	POL	993	14296	LLWKGEGAVV	95	100	111.1	632.4	25	770.8	3636.4	2
25.0142	10	NEF	219	14297	PLTFGWCFKL	61	74	142.8	741.4	4761.9	3700	47.6	2
1069.34	9	POL	993	14298	LLWKGEGAV	97	100	172.4	10750	21.7	1608.7	2666.7	2
25.0161	10	POL	452	14299	KLNWASQIYA	42	84	217.3	3909.1	400	6166.7	3076.9	2
1211.082	9	GAG	79	14300	SLYNTVATL	34	58	277.7	3583.3	50	37000	100000	2
25.0037	9	GAG	486	14301	FLQSRPEPT	44	68	454.5	10750	32.3	18500	3076.9	2
25.0046	9	POL	91	14302	TLWQRPLVT	61	68	270.2	21500	2500	18500	2857.1	1

TABLE XXVIII

in vitro binding of conserved HIV derived peptides to HLA-A3 supertype alleles

peptide	AA	protein	1st Position	Seq ID	sequence	Conservation (%)		A3-supertype binding capacity (IC50 nM)					alleles bound
						total	B	A*0301	A*1101	A*3101	A*3301	A*6801	
1273.01	9	GAG	163	14303	MVHQAISPR	42	58	61.1	89.6	18.0	13.8	9.5	5
1193.0200	9	POL	572	14304	IVIWGKTPK	75	79	129.4	16.2	18.2	96.7	242.4	5
1193.03	9	POL	931	14305	AVFIHNFKR	97	100	64.7	3.3	5.1	107.4	4.2	5
1193.01	9	POL	724	14306	YLAWVPAHK	34	95	142.9	105.3	327.3	33.0	2.0	5
1211.32	10	POL	971	14307	KIQNFRVYYR	81	95	343.8	28.6	2.7	341.2	210.5	5
1069.49	10	POL	929	14308	QMAVFIHNFK	94	100	9.2	8.5	268.7	432.8	400.0	4
1273.03	10	GAG	162	14309	QMVHQAISPR	42	58	42.3	6000.0	243.2	290.0	186.0	4
1193.09	9	POL	353	14310	MTKILEPFR	67	84	13750.0	375.0	81.8	69.0	25.8	4
966.01	9	POL	347	14311	AIFQSSMTK	56	79	10.0	10.0	12000.0	96666.7	242.4	3
940.03	10	NEF	100	14312	QVPLRPMTYK	72	79	18.0	9.5	1836.7	2230.8	133.3	3
1069.43	10	ENV	48	14313	TVYYGVPVWK	64	95	11.0	3.5	1636.4	10357.1	14.5	3
1069.48	10	POL	931	14314	AVFIHNFKRK	91	100	114.6	20.7	1125.0	5000.0	307.7	3
1273.05	9	POL	99	14315	TIKIGGQLK	27	63	40.7	181.8	18000.0	36250.0	72.7	3
1273.06	9	ENV	64	14316	TLFCASDAK	81	84	118.3	11.3	10588.2	22307.7	190.5	3
1273.07	10	ENV	61	14317	TTLFCASDAK	78	84	119.6	27.3	9473.7	14500.0	140.4	3
1273.04	9	ENV	878	14318	RIVELLGRR	34	89	200.0	600.0	138.5.	13809.5	444.4	3
1273.09	10	POL	98	14319	VTIKIGGQLK	27	63	297.3	28.6	10588.2	11600.0	125.0	3
1273.02	9	POL	246	14320	NTPVFAIKK	58	94.7	333.3	100.0	30000.0	48333.3	4.7	3
1150.14	9	POL	930	14321	MAVFIHNFK	94	100	647.1	20.0	375.0	517.9	2.5	3
1273.08	9	VIF	7	14322	VMIVWQVDR	69	95	3235.3	272.7	3.8	5.3	2424.2	3
1069.47	11	ENV	47	14323	VTVYYGVPVWK	64	94	84.6	11.3	4615.4	36250.0	170.2	3
1069.42	11	POL	722	14324	KVYLAWVPAHK	32	89	3.5	7.6	163.6	3580.2	8000.0	3
1069.44	9	POL	855	14325	KLAGRWPVK	78	68	8.5	133.3	500.0	72500.0	80000.0	3

TABLE XXIX

in vitro binding of conserved HIV derived peptides to HLA-B7 supertype alleles

peptide	AA	protein	1st Position	Seq ID	sequence	Conservation (%)		B7-supertype binding capacity (IC50 nM)					bound
						total	B	B*0702	B*3501	B*5101	B*5301	B*5401	
1146.01	9	NEF	94	14326	FPVRPQVPL	75	74	15.7	43.0	11.6	481.9	71.4	5
1296.01	9	ENV	259	14327	IPIHYCAPA	56	42	423	343	153	-	3.7	4
15.0268	10	GAG	545	14328	YPLASLRSLF	15	32	392.9	480.0	39.3	150.0	714.3	4
1261.01	9	POL	186	14329	FPISPIETV	88	95	3437.5	1043.5	148.6	251.4	9.1	3
1296.02	9	ENV	250	14330	CPKVSFEPI	47	79	100.0	5142.9	161.8	2447.4	100.0	3
1296.03	11	POL	893	14331	IPYNPQSQGVV	92	89	458.3	72000.0	119.6	46500.0	66.7	3
29.0028	8	REV	75	14332	VPLQLPPL	56	68	112.2	6000.0	0.8	46500.0	270.3	3
1292.13	9	GAG	237	14333	HPVHAGPIA	30	74	50.0	11.6	13750.0	4428.6	4.3	3

Table XXX: A1-motif peptides

Peptide	Seq ID	Sequence	Protein	Conservancy		1C50 nM
				Total	Clade B	
1.0431	14334	EVNIVTDSQY	HIV pol 1187	83	93	472
1.0014	14335	FRDYVDRFY	HIV gag 298	51	96	278
2.0129	14336	IYQYMDDLY	HIV pol 359	78	87	391
1069.27	14337	VIYQYMDDLY	HIV pol 358	78	87	446
1069.26	14338	VTVLDVGDAY	HIV pol 265	96	93	439

Table XXXI: A24-motif peptides

Peptide	Seq ID	Sequence	Protein	Conservancy		1C50 nM
				Total	Clade B	
25.0113	14339	IWGCSGKLI	HIV env 69	69	91	444
25.0 127	14340	IYETYGDTW	HIV vpr 92	92	100	207
1069.60	14341	IYQEPFKNL	HIV pol 1036	74	87	444
25.0128	14342	PYNEWTLEL	HIV vpr56	56	71	86
25.0123	14343	PYNTPVFAI	HIV pol 74	74	100	387
1069.57	14344	RYLKDQQLL	HIV env 2778	40	53	43
1069.58	14345	RYLRDQQLL	HIV env 2778	23	32	52
1069.59	14346	TYQIYQEPPF	HLVpol 1033	78	93	67
25.0115	14347	VWKEATTTL	HIV env 47	47	85	400
25.0218	14348	VWKEATTTLF	HIV env47	47	85	44
25.02 19	14349	YWQATWIPEW	HIV pol 96	96	93	182

Table XXXII: Immunogenicity of A2-supertype cross-reactive binding peptides

Peptide	SEQ ID	Sequence	Protein	Conservancy		XRN	Immunogenicity	
				Total	Clade B		patients	transgenic
1261.14	14350	LTFGWCFKLV	HIV nef 221	55	74	5	0/1	0/6
1261.04	14351	LTFGWCFKL	HIV nef 221	61	74	4	4/12	3/3
1261.06	14352	YTAFTIPSI	HIV pol 316	58	68	5	0/1	0/6
1261.15	14353	MASDFNLPPV	HIV pol 774	39	68	5	1/15	2/6
1069.32	14354	VLAEAMSQV	HIV gag 386	52	74	5	6/19	3/3
1261.16	14355	CTLNFPISPI	HIV pol 182	94	100	5	0/1	1/6
1261.02	14356	LLQLTVWGI	HIV env 651	53	63	4	2/8	1/6
1261.13	14357	KLVGKLNWA	HIV pol 448	95	95	4	3/15	3/3
1211.04	14358	KLTPLCVTL	HIV env 134	85	95	4	2/12	2/6
1261.08	14359	ALVEICTEM	HIV pol 220	23	79	4	0/2	1/6
1261.11	14360	AIIRILQQL	HIV vpr 59	61	74	4	5/9	0/6
1261.09	14361	LVGPTPVNI	HIV pol 163	84	100	4	1/9	1/6
1261.12	14362	RILQQLLFI	HIV vpr 62	56	74	3	6/20	2/6
1261.05	14363	TLNFPISPI	HIV pol 183	97	100	3	1/7	0/6
1261.03	14364	MTNNPPIPV	HIV gag 271	31	89	3	2/17	4/6
1261.17	14365	KMIGGIGGFI	HIV pol 132	97	95	3	2/7	0/6
941.03	14366	ILKEPVHGV	HIV pol 498	64	79	3	8/19	3/6
1261.10	14367	RAMASDFNL	HIV pol 772	64	79	3	2/9	0/6
1261.07	14368	KAACWWAGI	HIV pol 879	49	79	3	1/8	0/6
1211.09	14369	SLLNATDIAV	HIV env 814	22	68	3		

Table XXXIII: Immunogenicity of HIV-derived A3-supertype peptides

Peptide	SEQ ID	Sequence	Protein	Conservancy		XRN	Immunogenicity	
				Total	Clade B		transgenic	patients
1211.32	14370	KIQNFRVYYR	HIV pol 971	81	95	5	4/6	
1193.02	14371	IVIWGKTPK	HIV pol 572	75	79	5	0/6	
1193.03	14372	AVFIHNFKR	HIV pol 931	97	100	5	3/6	
1069.49	14373	QMAVFIHNFK	HIV pol 929	94	100	4	3/6	
1150.14	14374	MAVFIHNFK	HIV pol 930	94	100	3	6/6	
1069.48	14375	AVFIHNFKRK	HIV pol 931	91	100	3	0/6	
1273.01	14376	MVHQAISPR	HIV gag 163	42	58	5	0/6	
1273.03	14377	QMVHQAISPR	HIV gag 162	42	58	4	0/6	
1193.01	14378	YLAWVPAHK	HIV pol 724	34	95	5	0/6	
1069.42	14379	KVYLAWVPAHK	HIV pol 722	32	89	3	6/6	
1193.09	14380	MTKILEPFR	HIV pol 353	67	84	4	0/8	
966.01	14381	AIFQSSMTK	HIV pol 347	56	79	3	5/6	1/6
940.03	14382	QVPLRPMTYK	HIV nef 100	72	79	3	0/6	6/10
1069.44	14383	KLAGRWPVK	HIV pol 855	78	68	3		
1273.02	14384	NTPVFAIKK	HIV pol 246	58	95	3	0/6	
1273.08	14385	VMIVWQVDR	HIV vif 7	69	95	3	0/6	
1273.04	14386	RIVELLGRR	HIV env 878	34	89	3		
1273.07	14387	TTLFCASDAK	HIV env 61	78	84	3	3/6	
1273.06	14388	TLFCASDAK	HIV env 62	81	84	3	0/6	
1273.09	14389	VTIKIGGQLK	HIV pol 98	27	63	3	6/6	
1273.05	14390	TIKIGGQLK	HIV pol 99	27	63	3	0/6	
1069.43	14391	TVYYGVPVWK	HIV env 48	64	95	3	28/33	
1069.47	14392	VTVYYGVPVWK	HIV env 47	64	94	3	6/6	

Table XXXV: cross-reactive HLA-DR binding peptides

Peptide	SEQ ID	Sequence	Protein	Binding capacity (IC50 nM)												DR Alleles bound
				DR1	DR2w2ß1	DR2w2ß2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	DR6w19	DR7	DR8w2	DR9	DR53	
27.0313	14393	KRWIILGLNKIVRMY	HIV gag 298	4.2	5.1	24	188	633	404	54	124	0.36	379	49	58		12
27.0354	14394	WEFVNTPPLVKLWYQ	HIV pol 596	7.2	222	2.1	13636	28	20	317	1355	90	15	350	39		10
27.0377	14395	QKQITKIQNFRVYYR	HIV pol 956	2.9	3.4	80	-	357	49	53	124	25	25	75	577		11
1280.03	14396	KVYLAWVPAHKGIGG	HIV pol 712	8.3	25	24	-	156	165	71	12598	2500	179	196	250		9
27.0311	14397	GEIYKRWIILGLNKI	HIV gag 294	82	138	225	-	1667	380	213	1656	98	192	63	536		9
27.0361	14398	EKVYLAWVPAHKGIG	HIV pol 711	3.6	21	4.9	3226	9.3	27	37	6478	3500	18	31	144		9
27.0297	14399	QHLLQLTVWGIKQLQ	HIV env 729	6.1	21	690	-	1316	345	2128	1064	350	44	907	375		8
27.0304	14400	QGQMVHQAISPRTLN	HIV gag 171	72	65	13	17647	60	400	-	-	412	455	7313	117		8
27.0344	14401	SPAIFQSSMTKILEP	HIV pol 335	357	217	667	-	3571	109	741	-	13	68	3267	33		8
F091.15	14402	IKQFINMWQEVGKAMY	HIV env 566	128	217	206	-	417	271	4878	-	1000	-	350	5769	104	8
27.0341	14403	FRKYTAFTIPSINNE	HIV pol 303	185	70	4167	-	294	136	1818	-	-	30	803	39		7
27.0364	14404	HSNWRAMASDFNLPP	HIV pol 758	33	-	125	-	11	15	95	-	4375	472	1960	872		7
27.0373	14405	KTAVQMAVFIHNFKR	HIV pol 915	161	650	690	-	909	452	182	18625	125	1786	1441	2586		7

A dash indicates IC50>20μM

Table XXXVI: DR3 binding peptides

Peptide	Seq ID	Sequence	Protein	DR3
35.0135	14406	YRKILRQRKIDRLID	HIV vpu 31	23
35.0131	14407	WAGIKQEFGIPYNPQ	HIV pol 874	300
35.0127	14408	EVNIVTDSQYALGII	HIV pol 674	732
35.0125	14409	AETFYVDGAANRETK	HIV pol 619	769
35.0133	14410	GAVVIQDNSDIKVVP	HIV pol 989	1000

TABLE XXXVII

Immunogenicity of HIV-derived DR-supermotif peptides

Peptide	Seq ID	Sequence	Protein	Conservation (%)		DR Alleles bound	Patient Immunogenicity
				total	clad B		
27.0313	14111	KRWIILGLNKIVRMY	HIV gag 298	85 [89][1]	94 [95]	12	3/13
27.0311	14112	GEIYKRWIILGLNKI	HIV gag 294	58 [86]	95 [95]	9	2/13
27.0354	14113	WEFVNTPPLVKLWYQ	HIV pol 596	79 [89]	84 [95]	10	3/13
27.0377	14114	QKQITKIQNFRVYYR	HIV pol 956	56 [67]	95 [95]	11	3/13
1280.03	14115	KVYLAWVPAHKGIGG	HIV pol 712	32 [34]	89 [95]	9	3/13
27.0361	14116	EKVYLAWVPAHKGIG	HIV pol 711	32 [34]	94 [95]	9	1/13
27.0304	14117	QGQMVHQAISPRTLN	HIV gag 171	41 [42]	52 [58]	8	4/13
27.0344	14118	SPAIFQSSMTKILEP	HIV pol 335	52 [59]	79 [78]	8	3/13
27.0341	14119	FRKYTAFTIPSINNE	HIV pol 303	59 [58]	68 [68]	7	3/13
27.0364	14120	HSNWRAMASDFNLPP	HIV pol 758	48 [67]	68 [79]	7	3/13
27.0373	14121	KTAVQMAVFIHNFKR	HIV pol 915	87 [95]	94 [100]	7	4/13

1: conservation of core region

Table XXXVIII. Candidate CTL Epitopes

Restriction	Peptide	Protein	Seq ID	Sequence
HLA-A2	1069.32	HIV gag 386	14122	VLAEAMSQV
"	1261.03	HIV gag 271	14123	MTNNPPIPV
"	1261.15	HIV pol 774	14124	MASDFNLPPV
"	1261.13	HIV pol 448	14125	KLVGKLNWA
"	1261.09	HIV pol 163	14126	LVGPTPVNI
"	941.03	HIV pol 498	14127	ILKEPVHGV
"	1261.07	HIV pol 879	14128	KAACWWAG
"	1261.17	HIV pol 132	14129	KMIGGIGGFI
"	1261.10	HIV pol 772	14130	RAMASDFNL
"	1261.05	HIV pol 183	14131	TLNFPISPI
"	1211.04	HIV env 134	14132	KLTPLCVTL
"	1261.02	HIV env 651	14133	LLQLTVWGI
"	1211.09	HIV env 163	14134	SLLNATDIAV
"	1261.04	HIV nef 221	14135	LTFGWCFKL
"	1261.11	HIV vpr 59	14136	AIIRILQQL
"	1261.12	HIV vpr 62	14137	RILQQLLFI
HLA-A3	1069.49	HIV pol 929	14138	QMAVFIHNFK
"	1069.42	HIV pol 722	14139	KVYLAWVPA
"	1211.32	HIV pol 971	14140	KIQNFRVYYR
"	1193.09	HIV pol 353	14141	MTKILEPFR
"	966.01	HIV pol 347	14142	AIFQSSMTK
"	1273.09	HIV pol 98	14143	VTIKIGGQLK
"	1273.07	HIV env 61	14144	TTLFCASDAK
"	1069.47	HIV env 47	14145	VTVYYGVPVV
"	940.03	HIV nef 100	14146	QVPLRPMTYK
"	1273.08	HIV vif 7	14147	VMIVWQVDR
"	1273.03	HIV gag 162	14148	QMVHQAISPF
HLA-B7	15.0268	HIV gag 545	14149	YPLASLRSLF
"	1292.13	HIV gag 237	14150	HPVHAGPIA
"	1261.01	HIV pol 186	14151	FPISPIETV
"	1296.03	HIV pol 893	14152	IPYNPQSQGV
"	1296.01	HIV env 259	14153	IPIHYCAPA
"	1296.02	HIV env 250	14154	CPKVSFEPI
"	1146.01	HIV nef 94	14155	FPVRPQVPL
"	29.0028	HIV rev 75	14156	VPLQLPPL
HLA-A1	1.0431	HIV pol 684	14157	EVNIVTDSQY
"	1.0014	HIV gag 317	14158	FRDYVDRFY
"	1069.27	HIV pol 368	14159	VIYQYMDDLY
"	1069.26	HIV pol 295	14160	VTVLDVGDA
HLA-A24	1069.60	HIV pol 533	14161	IYQEPFKNL
"	25.0123	HIV pol 244	14162	PYNTPVFAI
"	1069.59	HIV pol 530	14163	TYQIYQEPF
"	25.0219	HIV pol 597	14164	YWQATWIPEW
"	25.0113	HIV env 681	14165	IWGCSGKLI
"	1069.57	HIV env 671	14166	RYLKDQQLL
"	25.0115	HIV env 55	14167	VWKEATTTLF
"	25.0127	HIV vpr 46	14168	IYETYGDTW
"	25.0128	HIV vpr 14	14169	PYNEWTLEL

Table XXXIX: HTL Candidate Epitopes

Selection Criteria	Peptide	Seq ID	Sequence	Protein
DR	27.0313	14170	KRWIILGLNKIVRMY	HIV gag 298
	27.0354	14171	WEFVNTPPLVKLWYQ	HIV pol 596
	27.0377	14172	QKQITKIQNFRVYYR	HIV pol 956
	1280.03	14173	KVYLAWVPAHKGIGG	HIV pol 712
	27.0311	14174	GEIYKRWIILGLNKI	HIV gag 294
	27.0361	14175	EKVYLAWVPAHKGIG	HIV pol 711
	27.0297	14176	QHLLQLTVWGIKQLQ	HIV env 729
	27.0304	14177	QGQMVHQAISPRTLN	HIV gag 171
	27.0344	14178	SPAIFQSSMTKILEP	HIV pol 335
	F091.15	14179	IKQFINMWQEVGKAMY	HIV env 566
	27.0341	14180	FRKYTAFTIPSINNE	HIV pol 303
	27.0364	14181	HSNWRAMASDFNLPP	HIV pol 758
	27.0373	14182	KTAVQMAVFIHNFKR	HIV pol 915
DR3	35.0135	14183	YRKILRQRKIDRLID	HIV vpu 31
	35.0131	14184	WAGIKQEFGIPYNPQ	HIV pol 874
	35.0127	14185	EVNIVTDSQYALGII	HIV pol 674
	35.0125	14186	AETFYVDGAANRETK	HIV pol 619
	35.0133	14187	GAVVIQDNSDIKVVP	HIV pol 989